

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:03:48 ; Search time 30.82 Seconds  
(without alignments)  
1571.934 Million cell updates/sec

Title: US-09-692-504-1  
Perfect score: 3498  
Sequence: 1 MRGGRGAPFWLPLPKALL.....FLPTPEELGLGPPRPQVLA 636  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3498	100.0	636	2 JH0047	class I cytokinase
2	298.5	8.5	783	2 JH0329	granulocyte colony
3	292	8.3	863	2 C38252	granulocyte colony
4	277	7.9	837	2 A34898	granulocyte colony
5	268.5	7.7	771	2 B38252	granulocyte colony
6	250	7.1	918	2 A36337	membrane glycoprot
7	248	7.1	917	2 I49699	glycoprotein 130 -
8	226.5	6.5	918	2 A44257	interleukin-130
9	206.5	5.9	1097	2 S17308	leukemia inhibitor
10	206	5.9	1092	2 JX0312	differentiation-st
11	178	5.1	894	1 A41527	protein-tyrosine k
12	170	4.9	1711	1 A55148	protein-tyrosine k
13	164.5	4.7	1185	2 T46428	hypothetical prote
14	162.5	4.6	1197	2 T30581	neural cell adhesi
15	159	4.5	1825	2 T32828	hypothetical prote
16	155	4.4	942	2 S33251	protein-tyrosine k
17	154.5	4.4	880	2 S33743	protein-tyrosine k
18	151	4.3	1274	2 S55050	cardiac myosin-bin
19	151	4.3	1914	2 T42635	tenascin Y precurs
20	150	4.3	888	2 S23065	ufo protein - mous
21	150	4.3	1232	2 T43027	neural cell adhesi
22	147.5	4.2	800	1 S31575	interleukin-4 rece
23	147.5	4.2	1239	1 A32579	neuroglian - fruit
24	146	4.2	876	2 I49152	protein-tyrosine k
25	146	4.2	1691	1 D54689	protein-tyrosine-p
26	144	4.1	890	1 A53743	protein-tyrosine k
27	144	4.1	1894	2 C54689	protein-tyrosine-p
28	143.5	4.1	4135	2 T42629	tenascin-X - bovin
29	142.5	4.1	1898	2 S46216	leukocyte antigen-

ALIGNMENTS

RESULT 1

JW0047

class I cytokinase receptor precursor - human

N:Alternate names: WSX-1

C:Species: Homo sapiens (man)

C:Date: 17-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 21-Jul-2000

C:Accession: JW0047

R:Spencer, C.A.; Grant, F.J.; Baumgartner, J.W.; Presnell, S.R.; Schrader, S.K.; Yam

Biochem. Biophys. Res. Commun. 246, 82-90, 1998

A:Title: Cloning and characterization of a novel class I cytokine receptor.

A:Reference number: JW0047; MUID:98262921

A:Accession: JW0047

A:Molecule type: mRNA

A:Residues: 1-836 <SPR>

A:Cross-references: GB:AF053004; NID:g3153240; PIDN:AAC39755.1; PID:g3153241

A:Experimental source: brain

C:Genetics:

A:Map position: 19p13.11

C:Keywords: glycoprotein

F:1-32/Domain: signal sequence #status predicted <SIG>

F:515-540/Domain: transmembrane #status predicted <TM>

F:554-561/Domain: cytoplasmic #status predicted <CTP>

F:51.76.302.311.374.382.467/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 100.0%; Score 3498; DB 2; Length 636;

Best Local Similarity 100.0%; Pred. No. 1.7e-231;

Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRGGRGAPFWLPLPKALLPPLLWLFQTRPQGSAGPLQCYGVGPLGLNCSWEPLGLD 60

Db 1 MRGGRGAPFWLPLPKALLPPLLWLFQTRPQGSAGPLQCYGVGPLGLNCSWEPLGLD 60

Oy 61 GAPSELHLQSQKYSRKNKTQTAVAGRSWVAIPRQLTMSDKLLVMGTGKAGPLPPFPV 120

Db 61 GAPSELHLQSQKYSRKNKTQTAVAGRSWVAIPRQLTMSDKLLVMGTGKAGPLPPFPV 120

Oy 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180

Db 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180

Oy 181 PELKTIPTPVEIQDELEATGYKVGRCRMEKEEDLWGENSPILSFOTPPSPAKDWWVSG 240

Db 181 PELKTIPTPVEIQDELEATGYKVGRCRMEKEEDLWGENSPILSFOTPPSPAKDWWVSG 240

Oy 241 NLCTGPGGEEPLLKAPGPCVQVSKVFWVGGRELSPGEGITCCCSLIPSGAENARVSA 300

Db 241 NLCTGPGGEEPLLKAPGPCVQVSKVFWVGGRELSPGEGITCCCSLIPSGAENARVSA 300

Oy 301 VNATSWEPLTNLSLCLDSASAPRSVAVSSIAGSTELLVTWQPGPEPLEHVVDWARDGD 360

Db 301 VNATSWEPLTNLSLCLDSASAPRSVAVSSIAGSTELLVTWQPGPEPLEHVVDWARDGD 360

```
QY 361 PLEKLNVRPPGNLSALLPGNFTVGVYRITVAVSASGLASASSVWGFREELAPLVGP 420
|||||
Db 361 PLEKLNVRPPGNLSALLPGNFTVGVYRITVAVSASGLASASSVWGFREELAPLVGP 420
|||||
QY 421 TLRWLDAPPCTPAIANGVPRHOLRGHLTHYTLCAQSGTSPSCVMVSGNTQSVTLPLDL 480
|||||
Db 421 TLRWLDAPPCTPAIANGVPRHOLRGHLTHYTLCAQSGTSPSCVMVSGNTQSVTLPLDL 480
|||||
QY 481 PWGPCELWVTAFTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
|||||
Db 481 PWGPCELWVTAFTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
|||||
QY 541 RCYHLRHVLPWRWKEKVPDPANSSSGQPHMEQVPEAQPLGDLPILEVEEMPPPPWESS 600
|||||
Db 541 RCYHLRHVLPWRWKEKVPDPANSSSGQPHMEQVPEAQPLGDLPILEVEEMPPPPWESS 600
|||||
QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRQVLA 636
|||||
Db 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRQVLA 636
|||||
RESULT 2
granulocyte colony-stimulating factor receptor D7 precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
R:Accession: JH0329; S21608
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sol
J. Exp. Med. 172, 1559-1570, 1990
A>Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0329
A:Molecule type: mRNA
A:Residues: 1-783 <L>R>
A:Cross-references: GB:X55720; NID:g31698; PIDN:CAA39252.1; PID:g31699
A:Experimental source: placenta
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <M
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-783/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 8.5%; Score 298.5; DB 2; Length 783;
Local Similarity 22.5%; Pred. No. 9,7e-13;
hes 160; Conservative 75; Mismatches 250; Indels 227; Gaps 34;
QY 50 LNCWEPLGDLGAPSELHLSQKYSRN-KTQTVAV-----AAGRSWVAIPREQLTMSDKL 103
|||||
Db 140 LICOWEPGPTHLPTSTFLKSPKRCNCQTQGSILDCVPKQSQHCCIPRKHLLYQNM 199
|||||
QY 104 LVW-----GTAGQPLW-----PPVFNLETQKNAPRLG-----PDVDF 139
|||||
Db 200 GIWVQAEALGTSNPQLCDPMDVVKLEPPMLRTMDPSPEAPPAQGLQLCWEP----- 255
|||||
QY 140 SEDDPLEATVHMAPPTWPSHKVLICOF-HYRRQCEAAWLTLELPELKIPLTPVEIQDLLEL 198
|||||
Db 256 -----WQPGHLINQK-----CELRHKPKQGEASWALVG-----LPLEALQYEL 294
|||||
QY 199 -----ATGKVVYGRCRMEEDLWGEWSPTLSFTQTPPSAPK-----DYVWSGNLCGTPGGEE 250
|||||
Db 295 CGLLPATATVTLQIRCIRWPLPGHWSNDSFSLERLTTRAPTVRLDTW----- 341
|||||
QY 251 LLWKAPGCVQVSVKVFVWVGRELSPEGITCCCSLIPSGAEWARSVAVNATSNEP-- 308
|||||
Db 342 ---WRQ-----RQLDPRTVQLFWKVPVLEDSGRIOGY-VVSWRPSG 379
|||||
QY 309 -----LTNLS-----LVCLDSA---SAPRSVAVSSIAGST----- 335
|||||
Db 380 QAGAILPLCNLTSELSTFHLPSAEQVALVAYNASTSRPTVPVFSRSGPALTRUHAMA 439
|||||
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QY 336 ----ELLVTWQPGPGPBLEHVVDWARDGDPLEKLN--WVRLPPGNLSA--LLPNFTVGV 388
|||||
Db 440 ROPHSLSWGWEPNPWPQGVYVTEWGLGPPSASNSNKTWRMEQNGRATGFLLENIRPFQL 499
|||||
QY 389 YRITVTVASASGLASASSVWGFREELAPLVGPTLWRLQDAPPCTPAIANGVPRHOLRGH 448
|||||
Db 500 YEIVTPLYQDTMGPSORHYAYSQEMAPSHAPEL-HLKHIGKTWAOLEWVPEPELGKSP 558
|||||
QY 449 LTHYTLCAQSGTSPSCVMVSGNTQSVTLPLDPWGPCELW-----VTA 491
|||||
Db 559 LTHYTLFWTNAQNSQSAILNASSRGFVLHGLE--PASLYHHLMAASAGATNSVTL 616
|||||
QY 492 STRIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFL--GCGLSLATSGRCYHLRKH 548
|||||
Db 617 MTLTPBGS-----ELHI-----ILGLFGLLLLTCLCG---TAWLCCSPNRK 655
|||||
QY 549 VLPWRWKEKVPDPANSSSG-----QPHMEQVPEAQPLGDLPILEVEEMPPPP-- 595
|||||
Db 656 ---NPLWSPVDPFPAHSSSLGWSVPTIMEADAFQLPGGLGTPITKLTAVLEEDKKVPWESH 712
|||||
QY 596 -----VMESSQPAQATAP-LDSGYEKHFLPTPEELGGLGPPR 631
|||||
Db 713 NSSETCGLPTLVQTVYVLOGDPRAVSTQPSQSG-----TSDQ---AGPPR 754
|||||
RESULT 3
granulocyte colony-stimulating factor receptor precursor, long form - human
N:Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim
C:Species: Homo sapiens (man)
C>Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
R:Accession: C38252; A38252; JH0330; A46486; S68332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A>Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348
A:Accession: C38252
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <FUK>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049
A>Note: Clones pHG11 and pHG5
A:Accession: A38252
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <FUK>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A>Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0330
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <FUK>
A:Cross-references: GB:X55721; NID:g31696; PIDN:CAA39253.1; PID:g31697
A>Note: clone 25-1; placenta
R:Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 148, 259-266, 1992
A>Title: Chromosomal gene organization of the human granulocyte colony-stimulating fa
A:Reference number: A46486; MUID:92091782
A:Accession: A46486
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 855-863 <SET>
A:Cross-references: GB:S71484; NID:g240883; PIDN:AAB20660.1; PID:g240884
A:Experimental source: granulocyte
A>Note: sequence extracted from NCBI backbone (NCBI:71484, NCBI:71485)
R:Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A>Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A:Reference number: S68331; MUID:96132662
```

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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:05:18 ; Search time 18.72 Seconds  
(without alignments)  
1245.664 Million cell updates/sec

Title: US-09-692-504-1

Perfect score: 3498

Sequence: 1 MRGGRGAPFWLPLKALL.....FLPTPEELGLGPPRPQVLA 636

Scoring\_table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	380	10.9	862	112S_HUMAN	Q99665 homo sapien
2	328.5	9.4	874	112S_MOUSE	P97378 mus musculus
3	297.5	8.5	836	GCGR_MOUSE	Q99062 homo sapien
4	277	7.9	837	GCGR_MOUSE	P40223 mus musculus
5	250	7.1	918	116B_MOUSE	P40189 homo sapien
6	248	7.1	917	116B_MOUSE	Q00560 mus musculus
7	236.5	6.5	918	116B_MOUSE	P40190 rattus norv
8	206.5	5.9	1097	116B_MOUSE	P42702 homo sapien
9	206	5.9	1097	116B_MOUSE	P42703 mus musculus
10	169.5	4.8	1711	PTPO_MOUSE	Q46112 rattus norv
11	160.5	4.6	887	UFO_MOUSE	P30530 homo sapien
12	157.5	4.5	1705	PTPO_MOUSE	P70289 mus musculus
13	155.5	4.4	1270	MYPC_MOUSE	O70468 mus musculus
14	154.5	4.4	880	TYO3_MOUSE	P55144 mus musculus
15	154.5	4.4	3067	CA1C_MOUSE	Q60847 mus musculus
16	151	4.3	1274	MYPC_MOUSE	Q14896 homo sapien
17	150	4.3	888	UFO_MOUSE	Q00993 mus musculus
18	147.5	4.2	1302	NRG_MOUSE	P20241 drosophila
19	146	4.2	4289	TENX_MOUSE	P22105 homo sapien
20	144	4.1	890	TYO3_MOUSE	Q06418 homo sapien
21	143.5	4.1	3063	CA1C_MOUSE	Q99715 homo sapien
22	142	4.1	880	TYO3_MOUSE	P55146 rattus norv
23	138.5	4.0	581	PLR_MOUSE	Q28172 bos taurus
24	137	3.9	1257	CAML_MOUSE	P32004 homo sapien
25	137	3.9	1284	NRCA_MOUSE	P35331 gallus gall
26	136	3.9	2944	CA17_MOUSE	Q02388 homo sapien
27	135	3.9	3164	TEGU_MOUSE	P10220 herpes simp
28	134.5	3.8	1162	LEPR_MOUSE	Q62959 rattus norv
29	134.5	3.8	1912	PTPD_MOUSE	P23468 homo sapien
30	133.5	3.8	1142	MYPC_MOUSE	Q14324 homo sapien
31	133	3.8	1266	NGCA_MOUSE	Q03696 gallus gall
32	133	3.8	1897	PTPE_MOUSE	P10586 homo sapien
33	132.5	3.8	1328	116B_MOUSE	Q91289 pleurodeles

RESULT	1	34	130.5	3.7	581	1	PLR_MOUSE	Q28235
112S_HUMAN		35	130.5	3.7	929	1	CA1C_MOUSE	Q91145 notophthalm
AC	Q99665	36	129	3.7	825	1	IL4R_MOUSE	P24394 homo sapien
DT	20-AUG-2001 (Rel. 40, Created)	37	129	3.7	1630	1	PTPL_MOUSE	P35992 drosophila
DT	20-AUG-2001 (Rel. 40, Last sequence update)	38	128.5	3.7	1259	1	CAML_MOUSE	O05695 rattus norv
DT	20-AUG-2001 (Rel. 40, Last annotation update)	39	128.5	3.7	1260	1	CAML_MOUSE	P11627 mus musculus
DE	INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-2) (IL-12R-BETA2).	40	128.5	3.7	2481	1	FINC_MOUSE	Q91740 xenopus lae
DE	2) (IL-12R-BETA2).	41	128	3.7	999	1	MERK_MOUSE	Q12866 homo sapien
OS	Homo sapiens (Human).	42	127.5	3.6	2029	1	LAR_MOUSE	P16621 drosophila
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	43	126.5	3.6	1138	1	TIEL_MOUSE	P35590 homo sapien
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	44	125	3.6	1131	1	MYPE_MOUSE	P16419 gallus gall
OX	NCBI_TaxID=9606;	45	124.5	3.6	1136	1	TIEL_MOUSE	Q08805 bos taurus
RN	[1]							
RP	SEQUENCE FROM N.A.							
RX	MEDLINE=97098510; PubMed=8943050;							
RA	Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,							
RA	Gately M.K., Gubler U.;							
RT	"A functional interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits."							
RL	Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).							
CC	-!- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A LOW AFFINITY.							
CC	-!- SUBUNIT: DIMER/OLIGOMER; DISULFIDE-LINKED. THE FUNCTIONAL HIGH AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND IL12RB2.							
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.							
CC	-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.							
CC	-!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.							
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).							
DR	EMBL; U64198; AAB36675.1; -							
DR	HSSP; P40189; LBQU.							
DR	MIN; 601642; -							
DR	InterPro; IPR002996; CRIA.							
DR	InterPro; IPR001777; FN_III.							
DR	InterPro; IPR003529; Hematopo_rcptor_L_F2.							
DR	Pfam; PF00041; fn3; 3.							
DR	SMART; SM00060; FN3; 3.							
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.							
KW	Receptor; Transmembrane; Glycoprotein; Signal; Repeat.							
FT	SIGNAL	1	21	POTENTIAL.				
FT	CHAIN	22	862	INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.				
FT	DOMAIN	22	624	EXTRACELLULAR (POTENTIAL).				
FT	DOMAIN	625	641	POTENTIAL.				
FT	DOMAIN	642	862	CYTOPLASMIC (POTENTIAL).				
FT	DOMAIN	224	306	FIBRONECTIN TYPE-III 1.				
FT	DOMAIN	421	508	FIBRONECTIN TYPE-III 2.				

## ALIGNMENTS

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FT DOMAIN 519 607 FIBRONECTIN TYPE-III 3.
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 862 AA; 97134 MW; 57C0E0D946B8DD58 CRC64;

Query Match 10.9%; Score 380; DB 1; Length 862;
Best Local Similarity 25.3%; Pred. No. 3.2e-19;
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGSAGPLOCYGVGLDNLNCWEPLGD-----LGARSELHLQSQ----- 71
DB 126 QPON-----LSCIOKGEQGTACTWGERGROTHLYTEVTLQSLGPKNLTWQCKDIYCDYL 181
QY 72 -----KYRSNKTQTV-AVAGRSWAIPREQLTMSDKLLVWGTAKAGOLPPPPVEVN 121
DB 182 DFGINLTPESPENFTAKVTAVNSLSSSSLP-STTFDIV-----RPL-PPWDIR 231
QY 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLEP 181
DB 232 IKFQ-KASVSR-----CTLYWR-----DEGLVLLNRLRYPSNSRLWN--- 269
QY 182 ELKTIPLTPV-----ETQDLELATYKVKYGRCRMEKEEDLWGENSPILSFQTP---PSAPK 234
DB 270 -----VNVTKAKGRHDLDLKPFTEYEQISSKLHLYKGSWSDSLESURAGTPPEEPTGML 325
QY 235 DVWVSGNLCTPGGEEPELLLWK-----APGPCVQVSYKVMFVWVGRELSP-----GITCCC 286
DB 326 DVWYMKRHIDY-SRQSLQSLFKWNLVSEARGKILHLYQVTLQELTGKAMTQNTIGHTSWT 384
QY 287 SLTPSGAEWA-RVSAVNA--TSHEPLTNLSLVCLDSASAPRSVAVSSIASTELLVTWQP 343
DB 385 TVIPRTGNNAVAVSAANSKGSILPTRINIMNLCEAGLLAPROVSANS-EGMDNILVTWQP 443
QY 344 ---GPGEPLEHVVDWAR---DGDPLEKLNWVRLPPGNLSALLPGNFTVGVPPYRITVTAVS 397
DB 444 PRKDPNAVQEVYVWEVRELHPGQGTQVPLNWRSLRPNVLSALISENTKSYCYEIRVYALS 503
QY 398 ASGLASSVWGFREELAPLVGLTLMRLQDAPGTPRAIMGEVPRHQLRGLHLYTIC-- 455
DB 504 GD-QGGCSSILGSKKAPLSGPHAINATE-EKGSILISNSIPVQEQMSCLLHYRIYWK 561
QY 456 -AQSQTSPVC---MNVSGNTQSVTLPLDLPWGPCELVWTASTTAGQGPPIRLHLPLDN 511
DB 562 ERDSNSQPLCEIPYRVSQNSHPINSLQ-PRVTYVLWMTALTAAGESSHGNEREFCL-QG 619
QY 512 TLRWK--VLPGL---LFLWGLFLGCGLSLATSGCYHLRHKVL-----PRWVWEKVP 559
DB 620 KANWMAFVAPSIATIMVGIF-----STHFQKVFVLLAALRPQWCSREIP 667
QY 560 DPANSSSGQPH-----MEQVPEAQLGDLPLILEVEEMEPVPPVMESSQPAQATA----PLD 610
DB 668 DPANSTCAKKYPIAEKTLPLDLRLDLWTPTE---DPEPLVISEVHLQVTPVERHPPC 723
QY 611 SGYEKHELPTPEELGLLG-----PPRQVVL 635
DB 724 SNMPQ-----REKGIQGHQASHKMDMHSSAPPPPRAL 756

RESULT 2
I12S_MOUSE
ID I12S_MOUSE STANDARD; PRT; 874 AA.
AC P97378;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-

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```

DE 2) (IL-12R-BETA2).
GN IL12RB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97098510; PubMed=8943050;
RA Presky D.H.; Yang H.; Minetti L.J.; Chua A.O.; Nabavi N.; Wu C.-Y.;
RA Gately M.K.; Gubler U.;
RT "A functional interleukin 12 receptor complex is composed of two
RT beta-type cytokine receptor subunits.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
CC -!- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
CC LOW AFFINITY.
CC -!- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; U64199; AAB36676.1; -.
DR HSSP; P40189; 1BQU.
DR MGD; MGI:1270861; IL12rb2.
DR InterPro; IPR002996; CRJA.
DR InterPro; IPR001777; FN.III.
DR InterPro; IPR003529; Hematopo_rcptor_L_F2.
DR Pfam; PF00411; fn3; 4.
DR PRINTS; PRO0014; PNTYPEIII.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
KW SIGNAL 1 20
FT CHAIN 21 874
FT DOMAIN 21 639
FT TRANSMEM 640 659
FT DOMAIN 657 874
FT DOMAIN 137 230
FT DOMAIN 240 322
FT DOMAIN 436 523
FT DOMAIN 534 622
FT CARBOHYD 48 48
FT CARBOHYD 101 101
FT CARBOHYD 114 114
FT CARBOHYD 142 142
FT CARBOHYD 151 151
FT CARBOHYD 169 169
FT CARBOHYD 179 179
FT CARBOHYD 224 224
FT CARBOHYD 252 252
FT CARBOHYD 279 279
FT CARBOHYD 287 287
FT CARBOHYD 323 323
FT CARBOHYD 391 391
FT CARBOHYD 495 495
FT SEQUENCE 874 AA; 98196 MW; 582E4D21BF1FBD67 CRC64;

Query Match 9.4%; Score 328.5; DB 1; Length 874;
Best Local Similarity 23.0%; Pred. No. 1.3e-15;
Matches 153; Conservative 91; Mismatches 268; Indels 153; Gaps 32;

QY 39 LQCYGVGPGDLNCSWEP-----LGDIGAPSELHLQSKYRSNKTQ----- 79

```

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:04:33 ; Search time 50.89 Seconds  
(without alignments)  
1828.045 Million cell updates/sec

Title: US-09-692-504-1  
Perfect score: 3498  
Sequence: 1 MRGGGAPFWLPLPKALL.....FLTPBELGLGPPRQVLA 636

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues  
number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_17.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3498	100.0	636	4 O60624	O60624 homo sapien
2	2044	58.4	623	11 O70394	O70394 mus musculu
3	326.5	9.3	861	6 O9BEG2	O9BEG2 bos taurus
4	292	8.3	971	11 O70458	O70458 mus musculu
5	288.5	8.2	970	11 O88821	O88821 mus musculu
6	241.5	6.9	918	13 O9W609	O9W609 gallus gall
7	237.5	6.8	881	13 O57519	O57519 xenopus lae
8	229	6.5	710	13 O57520	O57520 xenopus lae
9	226	6.5	979	4 O99650	O99650 homo sapien
10	212	6.1	1093	11 O70535	O70535 rattus norv
11	191	5.5	1236	4 O9UH13	O9UH13 homo sapien
12	191	5.5	1308	4 O9UH14	O9UH14 homo sapien
13	187.5	5.4	1180	4 O15051	O15051 homo sapien
14	180.5	5.2	1299	4 O15179	O15179 homo sapien
15	180	5.1	1299	4 O92823	O92823 homo sapien
16	173.5	5.0	1264	5 P91767	P91767 manduca sex
17	168	4.8	1154	11 O9QVN3	O9QVN3 rattus sp.
18	166.5	4.8	1146	13 O9I8V6	O9I8V6 gallus gall
19	166.5	4.8	1166	11 O9QVN4	O9QVN4 rattus sp.

20	166.5	4.8	1215	11	P97686	P97686 rattus norv
21	164.5	4.7	1185	4	Q9NTD2	Q9NTD2 homo sapien
22	163.5	4.7	1705	11	O9ERK5	O9ERK5 mus musculu
23	162.5	4.6	1197	13	O90478	O90478 brachydanio
24	161.5	4.6	1598	4	O9P214	O9P214 homo sapien
25	160	4.6	1148	13	Q9IBA7	Q9IBA7 gallus gall
26	159.5	4.6	4280	5	Q9UB29	Q9UB29 caenorhabdi
27	159.5	4.6	4450	5	Q9UB28	Q9UB28 caenorhabdi
28	156	4.5	1274	4	Q9UM53	Q9UM53 homo sapien
29	155.5	4.4	1147	13	Q9DDK1	Q9DDK1 meleagris g
30	151.5	4.3	2944	11	O63870	O63870 mus musculu
31	151	4.3	1914	13	Q91008	Q91008 gallus gall
32	150	4.3	890	11	Q9Z1A0	Q9Z1A0 cavia porce
33	150	4.3	1232	13	Q90284	Q90284 carassius a
34	147.5	4.2	800	11	O63257	O63257 rattus norv
35	147	4.2	1948	4	Q13332	Q13332 homo sapien
36	146	4.2	876	11	O60752	O60752 mus musculu
37	146	4.2	1894	11	O64487	O64487 mus musculu
38	146	4.2	4288	4	O9NPK9	O9NPK9 homo sapien
39	145.5	4.2	476	11	O9CU34	O9CU34 mus musculu
40	144	4.1	884	4	O14953	O14953 homo sapien
41	144	4.1	1399	4	O75870	O75870 homo sapien
42	143.5	4.1	4135	6	O18977	O18977 bos taurus
43	142.5	4.1	1898	11	O64604	O64604 r protein-t
44	141.5	4.0	1904	11	O64699	O64699 mus musculu
45	140.5	4.0	801	11	O9WTM8	O9WTM8 rattus norv

## ALIGNMENTS

RESULT 1  
O60624  
ID O60624 PRELIMINARY; PRT; 636 AA.  
AC O60624;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CLASS I CYTOKINE RECEPTOR (CRL1 PROTEIN).  
GN WSX1 OR CRL1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98262921; PubMed=9600072;  
RA Schreder C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,  
RA Schrader S.K., Yamagiwa T., Whitmore T.E., O'Hara P.J., Foster D.F.;  
RT "Cloning and characterization of a novel class I cytokine receptor.";  
RL Biochem. Biophys. Res. Commun. 246:82-90(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhang W., Wan T., He L., Yuan Z., Cao X.;  
RT "A novel gp130-like cytokine receptor.";  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF053004; AAC39755.1;  
DR EMBL: AF106912; AAG36090.1;  
DR InterPro: IPR003961; FN\_III.  
DR Pfam: PF00041; fn3; 2.  
DR SMART: SM00060; FN3; 1.  
SQ SEQUENCE 636 AA; 69473 MW; DC7DAAABA643CE97 CRC64;

Query Match 100.0%; Score 3498; DB 4; Length 636;  
Best Local Similarity 100.0%; Pred. No. 4.3e-251;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRGGGAPFWLPLPKALLPLLLVLFQTRPQGSAGPLQCYGVGPLGLNCSWEPLGDL 60  
Db 1 MRGGGAPFWLPLPKALLPLLLVLFQTRPQGSAGPLQCYGVGPLGLNCSWEPLGDL 60  
Qy 61 GAPSELHLQSQYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPPVPV 120

Db	61	GAPSELHQSQRYRSNKQTQVAAGRSGWVAPREQLTWSDKLLVWGTVKAGQPLPPPVFV	120
Qy	121	NLETMQNPNARLPGVDSEDPLEATVHWAPPPTWPSHKVLICOFHYRRCCOEAANTLLE	180
Db	121	NLETMQNPNARLPGVDSEDPLEATVHWAPPPTWPSHKVLICOFHYRRCCOEAANTLLE	180
Qy	181	PELKTIPLTVEIODLELATGYKVYGRCKMEBEDLWGSWSPILSFQTPPSPAKDVWVSG	240
Db	181	PELKTIPLTVEIODLELATGYKVYGRCKMEBEDLWGSWSPILSFQTPPSPAKDVWVSG	240
Qy	241	NLCSTPGCEBPLLWKAPGCVQSVKYVWFVWGGRELSPEGITCCCSLIPSGAEWARVSA	300
Db	241	NLCSTPGCEBPLLWKAPGCVQSVKYVWFVWGGRELSPEGITCCCSLIPSGAEWARVSA	300
Qy	301	VNATSWEPNLNSLVCLDSASAFRSVAVSSIAGSTELLTWOPGCGPELHVVDWARDGD	360
Db	301	VNATSWEPNLNSLVCLDSASAFRSVAVSSIAGSTELLTWOPGCGPELHVVDWARDGD	360
Qy	361	PLEKLNVRPLPNCNLSALLPGNFVTGVYPYRITVTVASGLASASVMGWGFREELAPLVGP	420
Db	361	PLEKLNVRPLPNCNLSALLPGNFVTGVYPYRITVTVASGLASASVMGWGFREELAPLVGP	420
Qy	421	TLWRLODAPGCTAIANGEVPRHQLRGHLTHYTLCQAQGSTSPVCNMVSGNTQSVTLPLD	480
Db	421	TLWRLODAPGCTAIANGEVPRHQLRGHLTHYTLCQAQGSTSPVCNMVSGNTQSVTLPLD	480
Qy	481	PWGCCELWVTASTAGOGPPGPIRLRLHPDLNTLRWKVLPGILFLMGLFLGCGLSLATS	540
Db	481	PWGCCELWVTASTAGOGPPGPIRLRLHPDLNTLRWKVLPGILFLMGLFLGCGLSLATS	540
Qy	541	RCYHLRHKVLPRWWEVKVPDPANSSSQPHMQEVPQAQPLGDLPILEVEEMPPPVMES	600
Db	541	RCYHLRHKVLPRWWEVKVPDPANSSSQPHMQEVPQAQPLGDLPILEVEEMPPPVMES	600
Qy	601	QPAQATAPLDSGYEKHFPLTPEELGGLGPPRPQVLA	636
Db	601	QPAQATAPLDSGYEKHFPLTPEELGGLGPPRPQVLA	636
RESULT	2		
O70394		PRELIMINARY;	PRT; 623 AA.
ID	O70394		
AC	O70394;		
DT	01-AUG-1998 (T-EMBLrel. 07, Created)		
DT	01-AUG-1998 (T-EMBLrel. 07, Last sequence update)		
DT	01-JUN-2001 (T-EMBLrel. 17, Last annotation update)		
DE	CLASS I CYTOKINE RECEPTOR.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OCX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98262921; PubMed=9600072;		
RA	Sprecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,		
RT	Schrader S.K., Yamagiwa T., Whitmore T.E., O'Hara P.J., Foster D.F.;		
RL	"Cloning and characterization of a novel class I cytokine receptor.,"		
DR	Biochem. Biophys. Res. Commun. 246:82-90(1998).		
DR	EMBL; AF053005; AAC40121.1; -		
DR	MGI; MGI:1355318; Wsx1.		
DR	InterPro; IPR003961; FN_III.		
DR	Pfam; PF00041; fn3; 1.		
DR	SMART; SW00060; FN3; 1.		
SQ	SEQUENCE 623 AA; 68998 MW; 4BA20FEFC875A7180 CRC64;		
Query Match	58.4%; Score 2044; DB 11; Length 623;		
Best Local Similarity	62.8%; Pred. No. 2.2e+143;		
Matches 388; Conservative	61; Mismatches 161; Indels 8; Gaps		
Qy	14	LPKLALPLLVLFQTRPQGSAGPLQCQYGVGPLGDLNGSWEPGLDGAAPSSEHLHSQRY	73

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Qy 39 LQCYGVGPGDGLNCSWEPLGD-----LGAPSELHLQSQ----- 71
Db 130 LSCIQKGERGTCTWHRGRDTHLYTAVTLQNLGPKNTWQKQNDHYCDHLGLINLTP 189
Qy 72 -KYRSNKT-OTVAVAGRSWAIPREQLTMSDKLLVWGTAKGQPLWPPVFNLETOMKPN 129
Db 190 BSLESSYTKVTAINSLGSASF-FSFTLLDIV-----RPL-PPWDRIKF----- 234
Qy 130 APRLGPVDSEDDPLEATVHWAPPTWPSHKVLICQHYRCQEAATLLEPELKTIPLT 189
Db 235 -----VNASVD-----RCTLWR-----DEGLVLLNRLRYRINRSNWNVN---VTNKG 277
Qy 190 PVEIQDLRELATGYKYVYGRCKEKEEDLNGENSPILSFOTPPSAP-----KDVW-----VSGN 241
Db 278 RHDLLDKPFTFEYEQISSKHLHYKGSWDSLSLRTQTPPEEPIGMLNVWYMRQHIDYN 337
Qy 242 LCGTPGGEPELHMK-----APGCVQVSYKVFVW-VGGRLESPGITCCCS---LIPS 291
Db 338 -----ROOISLFWKLNLSLSEARGKILH--YQVTLQKYGAGEITLQNTTEHTSWTWIPIR 389
Qy 292 CAEW-ARVSAVNA--TSMEPTNLISLVCLDSASAPRSVAVSSIAGSTELLVTWOP---GP 345
Db 390 TGNMAAVSAANSKSSLPTRINITDLGAEALPAQVLAKE-EGMDKLWWTWTPPEKAT 448
Qy 346 GEPLHVVWVARDGP-----LEKLNWRLPGLNLSALLPGNFTVGPYRITVAVSASGL 401
Db 449 AAVQEVVVEW-RELHPGAGMPPGLWLSPPYRLSALISENIKPYCIEIRVHAL-AGDQ 506
Qy 402 ASASVWGFEELAPLVGPTLWRLQDAPPTATANGVPRHQLRGLHTHYTLG-----AQS 458
Db 507 GGCSTRNSQHKAPLSPHNAISE-EKGSVLISWDBIPAREQMGCLHYRIYWKERDS 565
Qy 459 GTPSVC---MNVSGNTQSVTLPLDPMGPELWVTAAGQPPGPIRLHLPDNTLRW 515
Db 566 NSQPOLCEIPYRISNHPIDSLQ-PRVYVLMWLTALTAAGESQGNRECL-QGRANW 623
Qy 516 KVLPGILFLWGLFLGGLSLATSGRCYHLRHKL-----PRWVEKVPDPANSSSQPH 570
Db 624 STFVAPSTCMAMVWG-----VLSMRFRQKVFVLLALRPQWCKEIPDPANSTWAKY 678
Qy 571 MEQVPEAQPLGDLPILE---VEEMEP-----PP---VMSSQPAQA--T 606
Db 679 PIVEKTLQALDRLLTEWTPPEPEPLVINEVLCRVTPVFRPHRSWSEKGGVQGHYT 738
Qy 607 APLDSGYEKHFLPTP-----BELGLIG 629
Db 739 SEEDTGYSASSPPPPRAPTAETGQVDLYKVLGSKGP 775
RESULT 4
ID 070458 PRELIMINARY; PRT; 971 AA.
AC 070458:
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ONCOSTATIN M SPECIFIC RECEPTOR.
GN OSMR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98252923; PubMed=9584176;
RA Lindberg R.A., Juan T., Welcher A.A., Sun Y., Cupples R., Guthrie B.,
RA Fletcher F.A.;
RT "Cloning and characterization of a specific receptor for mouse
RT oncostatin M."
RL Mol. Cell. Biol. 18:3357-3367(1998).
DR ENBL; AF058805; AAC40122.1; -.
DR HSSP; P40189; 1BQU.

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DR MGI:1330819; Osmr.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
SQ SEQUENCE 971 AA; 110229 MW; BECAA85BBD47C1E7 CRC64;

Query Match      8.3%; Score 292; DB 11; Length 971;
Best Local Similarity 22.9%; Pred. No. 2.2e-13;
Matches 159; Conservative 87; Mismatches 275; Indels 174; Gaps 34;

Qy 50 LNCWEPLGDLGAPSELHLQSQKYR-----SNKTQTVAAAGRSWAIPREQ----- 96
Db 250 LDCSEPE---GVDTTLRKQRFQNYTLCSFSKCEVSNTYRNTYQITQEGSEMNF 305
Qy 97 -LTMDSKLLVWGTAKGQPLWPPVFNLETOMKPNAPRLGPDVDFSEDDPLEATVHWAPPT 155
Db 306 TLTAENQLKRKRSV-----INFNLTRVHPKAPQ---DVTLLIAGTKANWTWKVHS 354
Qy 156 WPSKVLICQHYRCQEAATLLEPELKTIPLTVEIQDLRELATGYKYVYGRCKEKEED 215
Db 355 HGNNYTLCCQVKLOYGE---VIHEHNVSVHMSANYLFSDLDPDTKYKAFVRCASANHFW 410
Qy 216 LWGEMSPILSFOTPPSAPK---DVMVSGNLGCTPGGEEPLLKWKAPGCVQ-----VS 265
Db 411 KWSMDTQ-KESTPBTAPSQALDWM--RQVWSENGRRIVTLFWK---PLLKSQANGKIIIS 464
Qy 266 YKVMFWVGRELSPEGITCCGLSIPSGAWEA-----VWAPALSTNLSDLDQPKIRITNNSGASP- 513
Db 465 YNI---VVENEAKPTESEHYC-----VWAPALSTNLSDLDQPKIRITNNSGASP- 513
Qy 310 TNLISLVCLDSASAPRSVAVSSIAGSTELL-VTWQPGCEPLEHVVDW-ARQGDPLEKLNW 367
Db 514 ---ESLWMLNSDSGHBEVEKTEKIGKIDAFNISWEPSVGDITMGVYVDWCAHSQDQCDLQW 571
Qy 368 VRLPPGNLSALLPG-NFTVGPYRITVAVSASGLAS-ASSVWGFREELAPLVGPTLWRL 425
Db 572 KNLGNTTSTITSDDFKPGVYRIFERSVEHVKARLVEKQRYTQELAPLVNPKV--- 628
Qy 426 QDAPPGTP---AIANGVEVPRHQLRGLHLYTLCAQS-----GTSPSVCMN 467
Db 629 -EIPYSTNSEVLRWPDYDSDFQAGFKGLVYVYKSKEMQCNQPWERTLLPDNSVLCKYD 687
Qy 468 VSGN-TQSVTLPD-L-PWGPCELWVTASTIAGQPPGPIRLHLPDNTLRWVLPGLFLW 525
Db 688 INGSETKTLTVENLQPELSLEYEFFVTPTYSAGPGNETFTKVTTPD--ARSHMLLIQLIPM 745
Qy 526 GLFLIGCLSLATSGRCYHLRHKLPRWVEK---VPDPANSS----- 565
Db 746 TLCVL---LSIIV---CYW-----KQWVKEKCYPDINPYKSSILSLIKSKKNPHILMN 794
Qy 566 -----SGQPHMEQVPEAQPLGDLPLEVEEMEPVPPVMESSQ 601
Db 795 VKDCIPDVLEVINKAEGSKTCVSGKGLHIEDVPTKPI--VP-TEKDSSGVPVPCIFPEN 851
Qy 602 PAQATAPLDSGYEKHFL-----PTPELGLLIGPP 630
Db 852 FTYDOSAFDSG--SHGLIPGLPKDTAHLQLGLLAPP 884

RESULT 5
O88821 PRELIMINARY; PRT; 970 AA.
ID O88821
AC O88821;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ONCOSTATIN M RECEPTOR BETA.
GN OSMR.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

RESULT	6
Q9W6U9	
ID	Q9W6U9
AC	Q9W6U9
DT	01-NOV
DT	01-NOV
DT	01-JUN
DE	GLYCOC
GN	GP130
OS	Gallus
OC	Eukary
OC	Archos
OC	Gallus
OX	NCBI_T
RN	[1]
RP	SEQUEN

Query Match 8.2%; Score 288.5; DB 11; Length 970;  
Best Local Similarity 22.6%; Pred. No. 4e-13;  
Matches 157; Conservative 89; Mismatches 275; Indels 173; Gaps 34;

Qy	50	LNCSEWPLGDLGAPSELUHLOSQYIR-----SNTQTQVAVAGRSWVAIPREQ-----	96
Db	250	LDCSWP---GVDTTLTWRKQFQNYLTCESEFSKRCESYNRNSYTWIQTIGSQEMYNF	305
Qy	97	-LTMSEDKLLVMGTKAGQPIWPPVFVNLEQTOMKNAPRLGPDVDFSEDDPLEATVHAPPT	155
Db	306	TLTAENQLRKRSVN-----NFNLTHRVHPKAPQ---DVTLLIIGATKANMTVKYHS	354
Qy	156	WPSHKVLCIOGHYRRCQEAAWTLLEBELKTIPTTPVEIOOLELATGYKYVGRCKMEKEBD	215
Db	355	HGNNYTTLLCQVKLOQYGB---VJHEHNVSVHMSANTLFSDLQDPDTKYKAFVRCASANHEW	410
Qy	216	LWGEWSPILFSQTPPPSAPK--DWVWSGNLCGTPGGEPLLLWKAPGPCVQ-----VS	265
Db	411	KWSOWTQ-KEFSTPETAPSQALUW--RQWSENGRRVITLFWK---PLLKSAQNGKIIIS	464
Qy	266	YKVMFWYGGRELSPGEGITCCCSJIPSGAEMA-----RVSAYNATSWEP	309
Db	465	YNI---VVENEAKPTSEHYC-----VMAPALSTNLSDLQPYKIRITANNMSGASP-	513
Qy	310	TNLSVLCLDSASAPRSVAVSSIAAGSTELLVTWQPGPELHVVDK--ARDGPLEKLKNW	368
Db	514	ESLMVLSNDSGEVKEKTIKIGIKDAFN--ISWEPVSGDITGYVVDCAHUSQQRCDLQWK	571
Qy	369	RLPPGNLSALLPG--NETVGVPYPIRITTVASASGLAS--ASSVMGFRBELAPLYGPTLWR	426
Db	572	NLGPNTTSTTTSDDFKPGVRYNFRIFERSVEHKARLQKQGYTQELAPLVNPKV----	627
Qy	427	DAPGCTP---AIANGEVPRHLQHLGHLTHYTLCAQS-----GTSPSVCMVN	468
Db	628	EIPYSTNSFVLRMPDYDSDFQAGFKGYLVVYKSKEMOCNPWERTLLPDNSVLCKYDI	687
Qy	469	SGN--TQSWTLPLDL--PMGPCSLWLTASTIAGQPGPGPILRLHPDNTLRWKVLPGILFLWG	526
Db	688	NGSETKTLTVENLOPESLYIEFFVTPTYTSAGPGNEFTTKVTPD--ARSHMLLOLILPMT	745
Qy	527	LFLGCGLSLATSRCRYHLRHKVLPRWWEK-----VPDPANSS-----	565
Db	746	LCVL---LSIIV---CYW-----KSQWVKECYDPIDPNPKYSILSKSNKPNHLMNV	794
Qy	566	-----SGOPHVEQVEAPQGLDPLTEVEEMEPVPVMESSQP	602
Db	795	KDCIPIOVLEINKAEGSKTCVCSGKLHIEDVETKPPI--VP--TEKDSGSPVPCIFFENF	851
Qy	603	AQATAPLDSGYEKHFL-----PTPEELGLLGGP	630
Db	852	TYDOSAFDGS--SHGLIPGPKUHTAOLGLAPP	883



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:03:48 ; Search time 43.01 Seconds  
(without alignments)  
1095.341 Million cell updates/sec

Title: US-09-692-504-1

Perfect score: 3498

Sequence: 1 MRGGRGAPFWLPLPKALL.....FLTPPEELGLGPPRPQVLA 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A: Geneseq\_1101.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
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19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	636	19 AAW33399	Alternatively spliced
2	3498	100.0	636	22 AAU01853	Human type I cyto
3	3490	99.8	636	20 AAY29781	Human DNAX cyto
4	3150	90.1	578	19 AAW33398	Human haematopoiet
5	2875	82.2	523	20 AAY29785	Partial human DNAX
6	2044	58.4	623	19 AAW33400	Mouse haematopoiet
7	2044	58.4	623	22 AAU01854	Mouse type I cyto
8	886.5	25.3	246	20 AAY29786	Partial mouse DNAX
9	400	11.4	150	20 AAY29782	Mouse DNAX cyto
10	380	10.9	862	18 AAW12771	Human interleukin-
11	298.5	8.5	783	12 AAR11741	Granulocyte colony

12	298.5	8.5	783	16	AAW77868	Human placental G-
13	298.5	8.5	783	18	AAW10485	Human granulocyte
14	297.5	8.5	800	18	AAW10486	Human granulocyte
15	297.5	8.5	801	12	AAR11742	Clone 25-1 encoded
16	297.5	8.5	813	21	AAB03873	Human granulocyte
17	297.5	8.5	836	12	AAR14255	Human GCSF recepto
18	293	8.4	873	22	AAU02905	Angiotensin conver
19	292	8.3	863	12	AAR14257	Human GCSF recepto
20	275	7.9	837	12	AAR14256	Murine GCSF recepto
21	268.5	7.7	771	12	AAR14256	Human GCSF recepto
22	268.5	7.7	824	22	AAR23678	Human EST encoded
23	251	7.2	917	13	AAW26334	gpi30. Mus muscul
24	250	7.1	918	15	AAW46233	Human soluble gly
25	250	7.1	918	21	AAW44694	Human gpi30 protei
26	249	7.1	775	22	AAU02904	Angiotensin conver
27	249	7.1	918	12	AAR10545	Recombinant human
28	248	7.1	708	17	AAR85911	gpi30 N-terminal f
29	248	7.1	917	21	AAW55073	Mouse gpi30 protei
30	247	7.1	918	17	AAW53368	Human gpi30 protei
31	235	6.7	708	14	AAR37804	Human gpi30 N-term
32	231.5	6.6	603	21	AAW32222	Granulocyte colony
33	226	6.5	979	17	AAR85912	Oncostatin M recep
34	218.5	6.2	961	21	AAW92187	Human gpi30-J-C-ga
35	217.5	6.2	951	20	AAW70798	Human gpi30-C-gamm
36	217.5	6.2	951	21	AAW92186	Human gpi30-C-gamm
37	210	6.0	658	17	AAW94576	Human gpi30 splice
38	207	5.9	662	22	AAB51244	Human haemopoietin
39	206.5	5.9	1097	15	AAW49508	Human LIF-R. Homo
40	206.5	5.9	1097	15	AAW45776	Human leukaemia in
41	206.5	5.9	1097	16	AAW74097	Human leukaemia in
42	205	5.9	1001	15	AAW45774	Human haemopoietin
43	204	5.8	652	22	AAB51242	Human haemopoietin
44	204	5.8	727	21	AAW92192	Human gpi30-kappa
45	204	5.8	738	21	AAW92194	Human gpi30-J-kapp

#### ALIGNMENTS

RESULT 1  
AAW33399  
ID AAW33399 standard; Protein; 636 AA.  
XX  
AC AAW33399;  
XX  
DT 22-MAY-1998 (first entry)  
XX  
DE Alternatively spliced zcytor1.  
XX  
KW Human; haematopoietic cytokine receptor; Zcytor1; ligand detection;  
KW cancer diagnosis; agonist; antagonist; alternatively spliced.  
XX  
OS Homo sapiens.  
XX  
PN WO9744455-A1.  
XX  
PD 27-NOV-1997.  
XX  
PF 19-MAY-1997; 97WO-US08502.  
XX  
PR 23-MAY-1996; 96US-0653740.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;  
XX  
DR WPI; 1998-018509/02.  
DR N-PSDB; AAT94120.  
XX  
PT Haematopoietic cytokine receptor - useful for ligand detection, and  
PT pathological condition diagnosis  
XX  
PS Claim 7; Pages 46-51; 86pp; English.



XX 18-OCT-2000; 2000WO-US28827.  
XX  
XX  
XX 20-OCT-1999; 99US-0160542.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX De Sauvage FJ, Grewal I, Gurney AL;  
XX  
XX WPI; 2001-308474/32.  
XX  
XX N-PSDB; AAS03262.  
XX  
XX Modulating T-cell differentiation and cytokine release profiles into  
XX Th1 and Th2 subtypes, for treating immune-related diseases in mammals,  
XX by administering modulator of type I cytokine receptor (TCR) -  
XX  
XX Example 1; Fig 3; 126pp; English.  
XX  
XX The sequence represents human type I cytokine receptor, hTCR. The  
XX invention relates to methods of modulating the differentiation of  
XX T-cells into the Th2 subtype instead of the Th1 subtype, by  
XX administering a modulator of TCR (e.g. an antagonist) to enhance,  
XX stimulate or potentiate T-cell differentiation, or using TCR  
XX polypeptide or its agonists to prevent, inhibit or attenuate T-cell  
XX differentiation. Th1 mediated disease in mammal can be treated by  
XX administering a TCR antagonist and Th2 diseases by administering a TCR  
XX agonist. Th1-mediated diseases include allograft rejection and autoimmune  
XX inflammatory diseases, such as allergic encephalomyelitis, multiple  
XX sclerosis, insulin-dependent diabetes mellitus, autoimmune uveoretinitis,  
XX inflammatory bowel disease or autoimmune thyroid disease. Th2-mediated  
XX diseases include infectious diseases, such as Leishmania major,  
XX Mycobacterium leprae, Candida albicans, Toxoplasma gondii, respiratory  
XX syncytial virus and human immunodeficiency virus (HIV) and allergic  
XX disorders, such as asthma, allergic rhinitis, dermatitis and vernal  
XX conjunctivitis.  
XX  
XX SQ Sequence 636 AA;

Query Match 100.0%; Score 3498; DB 22; Length 636;  
Best Local Similarity 100.0%; Pred. No. 2e-265;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGCGAPFWLWPKLALLLWLVLFQTRPQCSAGPLQCYGVGPGDGLNCSWEPLGDL 60  
DB 1 mrggagpfwlwpkallllwlvlfqtrpqsagplqcygvgpgldlncswepigdl 60  
QY 61 GAPSELHLQOKYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPPVFV 120  
DB 61 gapsehlhlokyrsnktqtvaagrswwaipreqltmsdkllvwtgkagqplwppvf 120  
QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICOFHYRRCOEAAWTLLE 180  
DB 121 nletqmknpaprlgpdvdfseddpleatvhwapptwpskhvlicofhyrrcqeawtlle 180  
QY 181 PELKTIPLTPEIQLDELATGKYVGRCKMEKEDLNGESWSPILSFQTPPSAPKDVWVSG 240  
DB 181 pelktipltpeiqldelatgkyvgrckmekeedlwgeswspilsfqtppsapkdvwvsg 240  
QY 241 NLCSTPGGEPLLLKAPGCVQVYKWFVWVGRELSPGEGITCCSLIPSGAEWARVSA 300  
DB 241 nlcstpggeeplllwkapgcvqvykwwfvwvgrlspggitccslipsgaewarvsa 300  
QY 301 VNATSWEPNLNLVCLDSASAPRSVSVSSTAGSTELLVTWQPGEPLEHVVDWARDGD 360  
DB 301 vnatswepnlslvcldsasaprsvsstagsstellvtwqpgpeplehvvwardgd 360  
QY 361 PLEKLNWRLPPGNLSALLPGNFVGPYRTVTAVASGLASSVWGVGFREELAPLVGP 420  
DB 361 pleklnwrlppgnlsallpgnftvgpyrtvtavasgllssvswgvgfrelaplvgp 420  
QY 421 TLWLQDAPPTGAPTAIANGVPRHQLRGLHTYLCAQSGTSPSCVMVSGNTQSVTLPLDL 480  
DB 421 tlwlqdappgtaiangevprhqlrghlthylcaqsgtspscvmvsgntqsvtlpdl 480

DB 421 tlwrlqdappgtaiangevprhqlrghlthylcaqsgtspscvmvsgntqsvtlpdl 480  
QY 481 PWGPCELWVTASTIAGQPPGPIRLHLPLDNTLRWKVLPGILFLAGLFLGGLSLATSG 540  
DB 481 pwgpcelwvtastiaaggppgpiirlhlpldntlrwkvlpigllflwglflgclslatsg 540  
QY 541 RCYHLRHVKVLPWWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVPMESS 600  
DB 541 rcyhlrhkvlprwwwekvpdpanssgqphmeqvpeaqplgdlpileveemepvpmess 600  
QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636  
DB 601 qpaqatapldsgyekhflptpeelgllgpprpqvla 636  
RESULT 3  
AAAY29781  
ID AAY29781 standard; Protein; 636 AA.  
XX  
AC AAY29781;  
XX  
DT 04-NOV-1999 (first entry)  
XX  
DE Human DNAX cytokine receptor subunit 1.  
XX  
KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
KW interleukin B30; DSRs1; DCRs1; IL-B30; cytokine receptor; diagnosis;  
KW inflammatory disorder; inflammatory response; innate immunity;  
KW morphogenic development; immunological disorder.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 108 /label= unknown  
FT /note= "encoded by AYT"  
XX  
PN WO9940195-A1.  
XX  
PD 12-AUG-1999.  
XX  
PF 05-FEB-1999; 99WO-US02600.  
XX  
PR 13-MAY-1998; 98US-0078194.  
PR 06-FEB-1998; 98US-0073941.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Kastelein RA, Mattson JD, McClanahan TK;  
XX  
DR WPI; 1999-527306/44.  
DR N-PSDB; AA208863.  
XX  
PT New receptor subunits useful in the treatment inflammatory disorders  
XX  
PS Claim 2; Page 14-17; 133pp; English.  
XX  
CC The present invention describes a composition (I) comprising DNAX  
CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
CC subunit I (DSRS1) protein, which together encode a new mammalian  
CC cytokine-related receptor (R), or DCRs1 and interleukin B30 (IL-B30)  
CC proteins, or DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRs1  
CC is useful for screening for ligands (i.e. agonists/antagonists) from  
CC a library of compounds, which are useful for modulating the physiology  
CC or development of a cell or tissue culture e.g. inflammatory responses,  
CC innate immunity and/or morphogenic development. (R), antibodies and  
CC ligands are useful for treatment of conditions, especially immunological  
CC disorders, associated with conditions exhibiting abnormal expression of  
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
CC and the subunits DSRs1 and DCRs1 are useful as immunogens for generating  
CC antibodies, or as antigens for binding antibodies. Nucleic acids  
CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
CC variants from other individuals or species. The present sequence

CC represents the specifically claimed human DCRS1; for use in the  
composition of the present invention.

XX Sequence 636 AA;

Query Match 99.8%; Score 3490; DB 20; Length 636;  
Best Local Similarity 99.7%; Pred. No. 8.3e-265;  
Matches 634; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGGGAPFWLWPKLALLPLLLWLFQRTPOGSGAPLQCYGVGGLDNCSEWPLGDL 60  
Db 1 mrgggagpflwlpkallplllwlfqtrpqgsagplqcygvglncswepldl 60  
QY 61 GAPSELHLQSQYRSNKTQTVAAGRSWVAIPREOLTMDSKLLVWGTKAGOPLPVPFV 120  
Db 61 gapsehlqsqyrsnktqtvaagrswwaipreqltmsdkllvwgkagpplvpfv 120  
QY 121 NLEQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180  
Db 121 nletqmkpnarlgpdrvdfseddpleatvhwappwpskhvllcqfhyrcqeaawtlle 180  
QY 181 PELKTIPLTPVEIQDLLELATGYKVGRCRMEKEEDLWGEWSPILSFQTPSPAPKDVWVSG 240  
Db 181 pelktipltpveiqdllelatgykvgrcrmekeedlwgespilsftqtppsapkdvwvsg 240  
QY 241 NLCGTPGGEPLLLWKAPGCVQVSYKVFVWVGGRLESPGEGITCCSLIPSGAEWARVSA 300  
Db 241 nlcgtpggeplllwkapgcvqvsykvvfwvggrelspggitccslipsgaeawarvsa 300  
QY 301 VNATSWEPITNLVLCLDSASAPRSVAVSIAGSTELLVWPGGEPLEHVVDWARDGD 360  
Db 301 vnatswepitnlvlcldsasaprsavavsiagstellvwpggeplehvmwardgd 360  
QY 361 PLEKLNWRLPPQNLISALLPGNFTVGPYRITVAVSASGLASASVWGFREELAPLVGP 420  
Db 361 pleklnwrlppqnlisallpgnftvgpyritvavssaglasasvwwgfrelaplvgp 420  
QY 421 TLWRLQDAPPGTPTAIWGEVPRHQLRGHHTHYTLCAQSGTSPSCVNMVSGNTQSVTLPLD 480  
Db 421 tlwrlqdappgtptaiwgevprrhqlrghthtytlcaqsgtspscvnmvsgntqsvtlpld 480  
QY 481 PNGPCBELWVASTIAGQGGPPGPIRLRHLPDNTLRWKVLPGLFLWGLFLGCGLSLATS 540  
Db 481 pngpcbelwvastiagqggppgirllrhlpdntlrwkvlpglflwglflgcglsats 540  
QY 541 RCYHLRHKVLPRWWEKVPDPANSSSQPHMQVPEAQPLGDLPILEVEEMEPVPVMESS 600  
Db 541 rcyhlrhkvlprwwekvpdpanssqphmqvpeaqplgdlpileveemepvpvme 600  
QY 601 QPAQATAPLDGSGYKHFLETPETLGLGPPRPQVLA 636  
Db 601 qpaqatapldsgykhfletpetlglgpprpqvla 636

RESULT 4

AAW33398  
ID AAW33398 standard; Protein; 578 AA.

XX AAW33398;

XX 22-MAY-1998 (first entry)

XX Human haematopoietic cytokine receptor zcytor1.

XX Human; haematopoietic cytokine receptor; zcytor1; ligand detection;  
XX Cancer diagnosis; agonist; antagonist.

XX Homo sapiens.

XX WO9744455-A1.

XX 27-NOV-1997.

XX 19-MAY-1997; 97WO-US08502.  
XX 23-MAY-1996; 96US-0653740.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;  
XX WPI: 1998-018509/02.  
XX N-PSDB; AAT94119.  
XX Haematopoietic cytokine receptor - useful for ligand detection, and  
XX pathological condition diagnosis  
XX Claim 1; Pages 39-43; 86pp; English.  
XX The present sequence is the human haematopoietic cytokine  
XX receptor zcytor1, useful for ligand detection, and pathological  
XX condition diagnosis, including cancer. Receptor agonists of the  
XX protein can be used to stimulate the proliferation and development  
XX of target cells in vitro and in vivo. The agonists can stimulate  
XX cell mediated immunity and lymphocyte proliferation, to treat  
XX infection involving immunosuppression, e.g. viral infections. They  
XX may also be used to suppress tumours, induce cytotoxicity, treat  
XX leukopaenias and enhance the regeneration of the T-cell repertoire  
XX after bone marrow transplantation. Antagonists of the protein may  
XX be used to suppress the immune system, treat autoimmune diseases,  
XX including rheumatoid arthritis, multiple sclerosis and diabetes  
XX mellitus. Immune suppression caused by the antagonists can also be  
XX used to reduce rejection of tissue or organ transplants and grafts,  
XX and to treat T-cell specific leukaemias and lymphomas.  
XX Sequence 578 AA;

Query Match 90.1%; Score 3150; DB 19; Length 578;  
Best Local Similarity 90.9%; Pred. No. 3e-238;  
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

QY 1 MRGGGAPFWLWPKLALLPLLLWLFQRTPOGSGAPLQCYGVGGLDNCSEWPLGDL 60  
Db 1 mrgggagpflwlpkallplllwlfqtrpqgsagplqcygvglncswepldl 60  
QY 61 GAPSELHLQSQYRSNKTQTVAAGRSWVAIPREOLTMDSKLLVWGTKAGOPLPVPFV 120  
Db 61 gapsehlqsqyrsnktqtvaagrswwaipreqltmsdkllvwgkagpplvpfv 120  
QY 121 NLEQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180  
Db 121 nletqmkpnarlgpdrvdfseddpleatvhwappwpskhvllcqfhyrcqeaawtlle 180  
QY 181 PELKTIPLTPVEIQDLLELATGYKVGRCRMEKEEDLWGEWSPILSFQTPSPAPKDVWVSG 240  
Db 181 pelktipltpveiqdllelatgykvgrcrmekeedlwgespilsftqtppsapkdvwvsg 240  
QY 241 NLCGTPGGEPLLLWKAPGCVQVSYKVFVWVGGRLESPGEGITCCSLIPSGAEWARVSA 300  
Db 241 nlcgtpggeplllwkapgcvqvsykvvfwvggrelspggitccslipsgaeawarvsa 300  
QY 301 VNATSWEPITNLVLCLDSASAPRSVAVSIAGSTELLVWPGGEPLEHVVDWARDGD 360  
Db 301 vnatswepitnlvlcldsasaprsavavsiagstellvwpggeplehvmwardgd 360  
QY 361 PLEKLNWRLPPQNLISALLPGNFTVGPYRITVAVSASGLASASVWGFREELAPLVGP 420  
Db 361 pleklnwrlppqnlisallpgnftvgpyritvavssaglasasvwwgfrelaplvgp 420  
QY 421 TLWRLQDAPPGTPTAIWGEVPRHQLRGHHTHYTLCAQSGTSPSCVNMVSGNTQSVTLPLD 480  
Db 421 tlwrlqdappgtptaiwgevprrhqlrghthtytlcaqsgtspscvnmvsgntqsvtlpld 480  
QY 481 PNGPCBELWVASTIAGQGGPPGPIRLRHLPDNTLRWKVLPGLFLWGLFLGCGLSLATS 540

Db	481	pwgpcelwvwtastiaaggpppirlrhlpdnrlrkwlpigllfllwglflgoglsiatsg	540
Qy	541	RCYHLRHKVLPRVWEKVPDPNASSSGQHQMEQVFAQPLGLDLPLEVEEMPPPPVMESS	600
Db	541	rcyhllrthkvlprvwkvpdpansss-----	566

RESULT 5

AY29785  
ID AY29785 standard; Protein: 523 AA.

DT 04-NOV-1999 (first entry)

Partial human DNAX cytokine receptor subunit 1.

KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
 KW interleukin B30; DSRF1; DCRF1; IL-B30; cytokine receptor; diagnosis;  
 KW inflammatory disorder; inflammatory response; innate immunity;  
 KW morphogenic development; immunological disorder.

OS Homo sapiens.

PN WO9940195-A1.

PD 12-AUG-1999.

PF 05-FEB-1999; 99WO-US02600.

PR 13-MAY-1998; 98US-0078194.

PR 06-FEB-1998; 98US-0073941.

PA (SCHE ) SCHERING CORP.

PI Kastelein RA, Mattson JD, McClanahan TK;

DR WPI; 1999-527306/44.

DR N-PSDB; AAZ08867.

PT New receptor subunits useful in the treatment inflammatory disorders  
XX  
PS Disclosure; Page 10-13; 133pp; English.

The present invention describes a composition (I) comprising DNAX cytokine receptor subunit 1 (DCRS1) protein and DNAX soluble receptor subunit 1 (DSRS1) protein, which together encode a new mammalian cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or DSRS1 and IL-B30 proteins. (I) comprising DCRS1 and DCRS1 is useful for screening for ligands (i.e. agonists/antagonists) from a library of compounds, which are useful for modulating the physiology or development of a cell or tissue culture e.g. inflammatory responses, innate immunity and/or morphogenic development. (R), antibodies and ligands are useful for treatment of conditions, especially immunological disorders, associated with conditions exhibiting abnormal expression of (R). (R) is useful as a phosphate labeling enzyme to label substrates, and the subunits DSR1 and DCRS1 are useful as immunogens for generating antibodies, or as antigens for binding antibodies. Nucleic acids encoding (R) are useful for identifying related DNAs and mRNAs, and variants from other individuals or species. The present sequence represents the partial human DCRS1, given in the present invention.

Sequence	523	AA:
----------	-----	-----

Query Match	82.2%;	Score 2875;	DB 20;	Length 523;
Best Local Similarity	99.6%;	Pred. No. 8.9e-217;		
Matches 521; Conservative	2;	Mismatches 0;	Indels 0;	

Qy	114	LWPVFVNLETQMKPNAPRGLGPDVDFSEDDPLEATVHMAPPTWPSHKVLICQPHYRRCOE	173
Db	1	WVPVFVNLETQMKPNAPRGLGPDVDFSEDDPLEATVHMAPPTWPSHKVLICQPHYRRCOE	60
Qy	174	AAWTLLEPELKTPLTPEVETQDLELATGYKVGRCRMEKEEDLWGSWPTLSFQTPPSAP	233
Db	61	AAWTLLEPELKTPLTPEVETQDLELATGYKVGRCRMEKEEDLWGSWPTLSFQTPPSAP	120
Qy	234	KDWVWSNGLCGTGGEBEPLLLXWAPGCVQVQYKVMFWGVBRELSPGEGITCCOCLIPSGA	293
Db	121	KDWVWSNGLCGTGGEBEPLLLXWAPGCVQVQYKVMFWGVBRELSPGEGITCCOCLIPSGA	180
Qy	294	EWARVSANVATSWEPITNLNLVCLDSASAPRSVAVSSISAGSTELLVTWQPGCEPLEHV	353
Db	181	EWARVSANVATSWEPITNLNLVCLDSASAPRSVAVSSISAGSTELLVTWQPGCEPLEHV	240
Qy	354	DWARDGDBLKNLRUPPNLGNFTVGVYRITVTAVSAGLASASVWGMFREE	413
Db	241	DWARDGDBLKNLRUPPNLGNFTVGVYRITVTAVSAGLASASVWGMFREE	300
Qy	414	LAPLVGPTLNRLODAPGTPAIAGVEPRHOLRGHHTVTLCAQSGTSPVCNMVSGNTQ	473
Db	301	LAPLVGPTLNRLODAPGTPAIAGVEPRHOLRGHHTVTLCAQSGTSPVCNMVSGNTQ	360
Qy	474	SVTLPLDLPWGCELWVTASTIAGQPPGPPIRLUHLPDNTLRNKLPGIIFLWGLFLGGC	533
Db	361	SVTLPLDLPWGCELWVTASTIAGQPPGPPIRLUHLPDNTLRNKLPGIIFLWGLFLGGC	420
Qy	534	LSLATSGRCYHLRHKVLPRWKEKVPDPANSSSQPHMEQVPEAPGLDPLILEVEEMP	593
Db	421	LSLATSGRCYHLRHKVLPRWKEKVPDPANSSSQPHMEQVPEAPGLDPLILEVEEMP	480
Qy	594	PPVMESSQPAQATAPLDSGYEKHFLLPTPEELGLLGGPPRPQVLA	636
Db	481	PPVMESSQPAQATAPLDSGYEKHFLLPTPEELGLLGGPPRPQVLA	523

## RESULT 6

AAW33400  
ID AAW33400 standard; Protein; 623 AA.

AAW33400:

22-MAY-1998 (first entry)

Mouse haematopoietic cytokine receptor Zcytor1.

Mouse; haematopoietic cytokine receptor; zcytor1; ligand detection;  
cancer diagnosis; agonist; antagonist; murine.

Mus sp.

PN WO9744455-A1.

PD 27-NOV-1997.

PF 19-MAY-1997; 97WO-US08502.

PR 23-MAY-1996; 96US-0653740.

PA (ZYMO) ZYMOGENETICS INC.

PI Baumgartner JW, Foster DC, Grant FJ, Sprecher CA:

DR WPI: 1998-018509/02.

DR N-PSDB; AAT94121.

PT - Haematopoietic cytokine receptor - useful for ligand detection, and  
PT pathological condition diagnosis

PS Claim 3; Pages 54-58; 86pp; English.





CC proteins, or DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRs1  
CC is useful for screening for ligands (i.e. agonists/antagonists) from  
CC a library of compounds, which are useful for modulating the physiology  
CC or development of a cell or tissue culture e.g. inflammatory responses,  
CC innate immunity and/or morphogenic development. (R), antibodies and  
CC ligands are useful for treatment of conditions, especially immunological  
CC disorders, associated with conditions exhibiting abnormal expression of  
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
CC and the subunits DSRs1 and DCRs1 are useful as immunogens for generating  
CC antibodies, or as antigens for binding antibodies. Nucleic acids  
CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
CC variants from other individuals or species. The present sequence  
CC represents the partial mouse DCRs1, given in the present invention.  
XX  
SQ Sequence 246 AA;

Query Match 25.3%; Score 886.5; DB 20; Length 246;  
Best Local Similarity 67.1%; Pred. No. 1.5e-61;  
Matches 165; Conservative 27; Mismatches 47; Indels 7; Gaps 2;  
QY 386 GVPYRTVTAVSAGSLASVYMGPREELAPLVGPTLWRLQDAPCTPAIANGVEVPRHOL 445  
DB 3 gpyrtvtavsgslasvymgpreelaplvgptlwrlqdadpctptaiangvevprhql 62  
QY 446 RGHLYHTLCAQSGTSPSCMVNSGNTQSVTLPLDPLWGPCELWVTAFTIAGQPGPIILR 505  
DB 63 rgqathytfcigrlstcrvnsqqtatipnlhsgsfklwvstvtvaggpgpddis 122  
QY 506 LHLPDNTLRKLVLPGLIFLWGLFLLGCGLSLATS-----GRCYHLRHKVLPRWWEKVPDP 561  
DB 123 lhlpdntrkvlpglflwglfllgclslatslrcqlgclhwrhklipqwiwervpdp 182  
QY 562 ANSSGQPMHGVPEAQPLGDLPILEVERMEPPVYMESSQPAQATAPLDGVEKHFLEPPT 621  
DB 183 ansnggpyikevslpqpdkdglleeeveqlpvvves---pkasapiysgyekhflepcp 239  
QY 622 EELGLL 627  
DB 240 eelgl 245

RESULT 9  
ID AAY29782  
XX AAY29782 standard; Protein; 150 AA.  
AC AAY29782;  
XX  
XX 04-NOV-1999 (first entry)  
DE Mouse DNAX cytokine receptor subunit 1.  
XX  
XX DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
KW Interleukin B30; DSRs1; DCRs1; IL-B30; cytokine receptor; diagnosis;  
KW inflammatory disorder; inflammatory response; innate immunity;  
KW morphogenic development; immunological disorder.  
XX  
XX Mus sp.

Key Location/Qualifiers  
FT Misc-difference 150  
FT /label= unknown  
FT /note= "encoded by GAN"

PN WO9940195-A1.  
XX  
XX 12-AUG-1999.  
XX  
XX 05-FEB-1999; 99WO-US02600.  
XX  
XX 13-MAY-1998; 98US-0078194.  
XX 06-FEB-1998; 98US-0073941.

PA (SCHE ) SCHERING CORP.  
XX Kastelein RA, Mattson JD, McClanahan TK;  
XX WPI; 1999-527306/44.  
DR N-PSDB; AAZ08864.  
XX  
PT New receptor subunits useful in the treatment inflammatory disorders  
XX  
PS Claim 2; Page 17-18; 133pp; English.  
XX  
CC The present invention describes a composition (I) comprising DNAX  
CC cytokine receptor subunit I (DCRs1) protein and DNAX soluble receptor  
CC subunit I (DSRs1) protein, which together encode a new mammalian  
CC cytokine-related receptor (R), or DCRs1 and interleukin B30 (IL-B30)  
CC proteins, or DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRs1  
CC is useful for screening for ligands (i.e. agonists/antagonists) from  
CC a library of compounds, which are useful for modulating the physiology  
CC or development of a cell or tissue culture e.g. inflammatory responses,  
CC innate immunity and/or morphogenic development. (R), antibodies and  
CC ligands are useful for treatment of conditions, especially immunological  
CC disorders, associated with conditions exhibiting abnormal expression of  
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
CC and the subunits DSRs1 and DCRs1 are useful as immunogens for generating  
CC antibodies, or as antigens for binding antibodies. Nucleic acids  
CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
CC variants from other individuals or species. The present sequence  
CC represents the specifically claimed mouse DCRs1, for use in the  
CC composition of the present invention.  
XX  
SQ Sequence 150 AA;

Query Match 11.4%; Score 400; DB 20; Length 150;  
Best Local Similarity 61.4%; Pred. No. 9.2e-24;  
Matches 78; Conservative 11; Mismatches 38; Indels 0; Gaps 0;  
QY 14 LPKLALLPLLVLFORTRPOGSAGPLQCYGVGPLDGLNCSWEPLDGLGAPSELHLSQSKY 73  
DB 23 ltpklellslmslllgttrphgspgplqcyvgplglncswepldgletppvlyhqsqky 82  
QY 74 RSNKQTQTVAVAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVFVNLETOMKPNAPRL 133  
DB 83 hpnrvwekvpskqswvtipreqftmadklllwgtdqgrplwssvsvnletqmkpdpqi 142  
QY 134 GPDVDFS 140  
DB 143 fsqvdls 149

RESULT 10  
AAW12771  
ID AAW12771 standard; Protein; 862 AA.  
XX  
AC AAW12771;  
XX  
DT 12-MAY-1997 (first entry)  
XX  
XX Human interleukin-12 beta-2 receptor.  
XX  
XX Interleukin-12 beta-2 receptor; IL-12; autoimmune disease;  
KW rheumatoid arthritis; inflammatory bowel disease;  
KW multiple sclerosis.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= Sig\_peptide 24..622  
FT Domain /label= Extracellular\_domain 623..646  
FT Domain /label= Transmembrane\_domain



FT Domain 647..862  
 FT /label= Cytoplasmic\_tail  
 FT Region 132..145  
 FT /label= Cytokine\_receptor\_motif  
 FT /note= "cytokine receptor superfamily motif  
 FT (Cys132..Cys139)"  
 FT Region 305..309  
 FT /label= Cytokine\_receptor\_motif  
 FT /note= "cytokine receptor superfamily motif  
 FT (W305SKWS)"  
 FT Modified-site 47..50  
 FT /label= N-linked\_glycosylation\_site  
 FT Modified-site 129..131  
 FT /label= N-linked\_glycosylation\_site  
 FT Modified-site 166..168  
 FT /label= N-linked\_glycosylation\_site  
 FT Modified-site 186..188  
 FT /label= N-linked\_glycosylation\_site  
 FT Modified-site 195..197  
 FT /label= N-linked\_glycosylation\_site  
 FT Modified-site 271..273  
 FT /label= N-linked\_glycosylation\_site  
 FT Modified-site 347..349  
 FT /label= N-linked\_glycosylation\_site  
 FT Modified-site 376..378  
 FT /label= N-linked\_glycosylation\_site  
 FT Modified-site 480..482  
 FT /label= N-linked\_glycosylation\_site  
 FT Modified-site 667..669  
 FT /label= Conserved\_box\_motif  
 FT /note= "conserved motif of cytokine receptor  
 FT superfamily"  
 FT Region 699..704  
 FT /label= Conserved\_box\_motif  
 FT /note= "conserved motif of cytokine receptor  
 FT superfamily"  
 FT Region 786..798  
 FT /label= Conserved\_box\_motif  
 FT /note= "conserved motif of cytokine receptor  
 FT superfamily"  
 FT EP759466-A2.  
 FT 26-FEB-1997.  
 FT 23-JUL-1996; 96EP-0111807.  
 FT 30-MAY-1996; 96US-0018674.  
 FT 01-AUG-1995; 95US-0001701.  
 FT (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 FT Gubler UA, Presky DH;  
 FT WPI: 1997-147515/14.  
 FT N-PSDB: AAT59731.

XX New interleukin-12 beta-2 receptor and high binding affinity  
 XX complexes - have a high affinity for Interleukin-12, and are used to  
 XX treat autoimmune diseases

PS Claim 3; Page 24-29; 53pp; English.

XX New human Interleukin-12 (IL-12) receptor beta-2 receptor (AAW12771)  
 CC has a low binding affinity for IL-12, but when complexed with an  
 CC IL-12 beta-1 receptor (see also AAW12772), forms a complex with a  
 CC high binding affinity for IL-12. Its amino acid sequence was  
 CC deduced from a composite cDNA sequence (AAT59731) obt'd. from human  
 CC lymphoblasts. IL-12 receptor beta-2 can be expressed on the  
 CC surface of transformed host cells, opt. as a complex with  
 CC co-expressed IL-12 receptor beta-1, and used in therapeutic  
 CC compns., pref. with at least 1 cytokine antagonist, to treat  
 CC autoimmune dysfunctions such as rheumatoid arthritis, inflammatory

CC bowel disease and multiple sclerosis. The receptor protein or  
 CC complex can also be used to detect (ant)agonists of IL-12 activity.  
 XX  
 SQ Sequence 862 AA;  
 Query Match 10.9%; Score 380; DB 18; Length 862;  
 Best Local Similarity 25.3%; Pred. NO. 3.5e-21;  
 Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;  
 QY 31 RQGSAGPLQCYGVGPGDLNCSWEPLGD-----LGAPSELHLSQ----- 71  
 DB 126 qpqn-----lsciqkgeqgtvactwergrdthlyteytlqslgsknltwgkdkdydyl 181  
 QY 72 -----KYRSNKTQTV-AVAAGRSWVAIPREQLTMSDKLLVMGTAGQPLWPPVFN 121  
 DB 182 dfglnltspesnftakvtavnslgssslp-sftflldiv-----rpl-ppwdir 231  
 QY 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQBAAWTLLEP 181  
 DB 232 ikfq-kasvsvr-----ctlywr-----degllvllnrlyrpsnsrlwm--- 269  
 QY 182 ELKTIPLTPV---EIQDELELATGYKVCRCRMEKEEDLNGEWSPLSFQTP---PSAPK 234  
 DB 270 ----vntckagrhdldlkpfteyefqlsskhllykgswwdseslraqtpeeeptgml 325  
 QY 235 DVWVSGNLCTGPGGEPLELLMK-----APGCVQVSVKVMFWMVGGRSLSPE--GTCC 286  
 DB 326 dwymkrhidy-srqqlsfwknlsvseargkilyqvtlqeltgkamtqhtswt 384  
 QY 287 SLIPSGAEN-A-RVSAVNA--TSWEPLTNLSLVCLDSASAPRSVAVSSVSTELVLTWQP 343  
 DB 385 tviprtgnwawavsaanskgspltrlnlniceagllaprqvsans-egmdnllvtwqp 443  
 QY 344 --GGEPLHVDWAR--DGDPLEKLNWRLPPGNLSALLPGNFTVGVPIRYTVAVS 397  
 DB 444 prkpsavqeyvvevrehphgtdtqvpnlwrsrpnvnsalisenikayicyeirvays 503  
 QY 398 ASGLASASSVMGFREELAPLVGPTLWRLQDAPPGTPAIAWGEVPRHQLRHLTHYTLG-- 455  
 DB 504 gd-qggcslilgnskhhkapsghinaite-ekgslilswnsipvqeqmgcllyriywk 561  
 QY 456 -AQGTSPSVC---MNVSGNTQSVTLPLDPLMGPCBLWVTASTIAGQGGPPGPIRLUHLDPN 511  
 DB 562 erdsnsqqlceipyrvsqnsphlnslq-prvtvylwmtaltaageshgnerefc-l-gg 619  
 QY 512 TLRWK--VLPGI---LFLWGLFLLCGLSLATSGRCYHLRHVKL-----PRWWEKVP 559  
 DB 620 kanmavfapslclailmvgif-----sthyfqkvfvlalalrpqwcseip 667  
 QY 560 DPANSSSQPH-----MEQVPEAQPLGDLPILEVEEMEPVPMVMSQPAQATA----PLD 610  
 DB 668 dpanstcakypiaeeektqlpldrilldwptpe---dpeplviseivlhqvtvfrhpc 723  
 QY 611 SGYEKHLPTPEELGLLG-----PPRPQVL 635  
 DB 724 snwbq-----rekgigghqasekdmmhsassppppral 756  
 RESULT 11  
 AAR11741  
 ID AAR11741 standard; Protein; 783 AA.  
 XX  
 XX AAR11741;  
 AC  
 XX  
 XX 04-JUL-1991 (first entry)  
 XX  
 DE Granulocyte colony stimulating factor receptor.  
 XX  
 KW G-CSF; receptor; clone D-7.  
 XX  
 OS Homo sapiens.  
 XX





Db 342 -----wrq-----rqlprtqlfwkvpbleedsgrlqgy-vvswrpsg 379  
QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335  
Db 380 qagallplcmtelstctfhlpsaeqavalvaynsagtsrtpvfvfesrgpaltrihama 439  
QY 336 -----ELLVTVQPGPGPLEHVVDWARDGPLEKLN--WVRLPPGNLSA-LLPGNFTVGVYP 388  
Db 440 rdphslwvgwepnpwpqgyvlewglgppsasnsnktwmeqngratgflkenirpfql 499  
QY 389 YRITVTAVSASGLASASSVWGFREELAPLVGPTLWRLQDAPGTPAIANGEVPRHQLRGH 448  
Db 500 yeiivtplyqdtmgsqhvayysqemashapel-hlkhigtwaqlewvpeppelgksp 558  
QY 449 LTHYTLCAQSGTSPSVCNMVSGNTQSVTLDPDLPWGPCELW-----VTA 491  
Db 559 lthytifwtanqgsfalsalnassrgfvlhgile--paslyhihlmaasqagatnstvltl 616  
QY 492 STIAGGPGPILRLHLPDNTLRWKVLPGLFLWGLFLL--GCGLSLATSGRCYHLRHK 548  
Db 617 mltltpgs-----elhi-----ilglfllllltclcg----tawlcspnrk 655  
QY 549 VLPRWVWEKVPDPANSSG-----QPHMEQVP--EAQPLGDLPTLEVEEMEP-- 595  
Db 656 ----nplwpsvdpahsigswwptimeedafqlpglgtptlktlvleedekkpvpwesh 712  
QY 596 -----VMESSQAQATAP-LDSGYEKHFLPTPEELGLLGPPR 631  
Db 713 nssetcglptlvqtylqgdpravstqpsqsg-----tsdq---aqppr 754  
  
RESULT 14  
AAW10486  
ID AAW10486 standard; Protein; 800 AA.  
XX AC AAW10486;  
XX DT 27-APR-1997 (first entry)  
XX DE Human granulocyte colony stimulating factor receptor.  
XX KW Granulocyte colony stimulating factor receptor; G-CSFR; diagnosis;  
XX KW therapy.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Peptide 1..24  
FT Protein /label= Sig\_peptide  
FT /label= Mat\_protein 25..783  
FT Domain 628..653  
FT /label= Transmembrane\_domain  
FT Misc-difference 750..800  
FT /note= "alternative C-terminal sequence"  
XX  
PN US5589456-A.  
XX  
PD 31-DEC-1996.  
XX  
PF 26-SEP-1989; 89US-0412816.  
XX  
PR 24-SEP-1990; 90US-0587329.  
PR 26-SEP-1989; 89US-0412816.  
PR 03-OCT-1989; 89US-0416306.  
PR 03-APR-1990; 90US-0522952.  
PR 15-JAN-1993; 93US-0006183.  
PR 02-FEB-1995; 95US-0382771.  
XX  
PA (IMV ) IMMUNEX CORP.  
XX  
PI Curtis KM, Larsen AD, Sims JE, Smith CA;  
XX

DR WPI; 1997-076879/07.  
DR N-PSDB; AAT47100.  
XX Recombinant granulocyte colony stimulating factor receptor - for  
PT diagnostic, therapeutic and research uses  
XX Claim 1; Fig 3; 15pp; English.  
XX An alternative form (AAW10486) of human granulocyte colony  
CC stimulating factor receptor (G-CSFR) (see also AAW10485) results  
CC from alternative splicing and a change in the reading frame,  
CC leading to a different C-terminal amino acid sequence. It is the  
CC product of a cDNA clone (AAT47100) isolated from a human placental  
CC library. Recombinant G-CSFRs, esp. soluble forms comprising the  
CC extracellular domain, or modified forms having inactivated  
CC N-glycosylation sites, altered KEX2 protease cleavage sites or  
CC conservative amid acid substns., can be produced in host cells.  
CC G-CSFR polypeptides are useful in diagnostic assays of G-CSF, and  
CC for raising antibodies of use in diagnosis and therapy. G-CSFR  
CC can also be used in therapy to bind or scavenge G-CSF.  
XX SQ Sequence 800 AA;  
  
Query Match 8.5%; Score 297.5; DB 18; Length 800;  
Best Local Similarity 22.8%; Pred. No. 9e-15;  
Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;  
  
QY 50 LNCSEPEPLDGLCAPSELHLOSOKYRSN-KTORVAV-----AAGRSWVAIPRQLTMSDKL 103  
Db 140 llicqewpethlptsftlksfksrgnoqtgqdsldcvpkdggshcciprkhllyqnm 199  
QY 104 LVW-----GTKAGQPLW-----PPVFVNLETKMKNAPRLG-----PDVDF 139  
Db 200 glwvqaenalgtspmqicldgmdvukleppmlrmdpeaappqagclqewp---- 255  
QY 140 SEDDPLEATVHWAPPTWPSHKVLICQF-HYRQCOBAWTLLEPELKTPLTPEVETQDL 198  
Db 256 -----wqpglhinqk---celrhkpkrgaeaswalvgp-----lplealqyel 294  
QY 199 -----ATGVKVVGRCKMEKEEDLWGEWSPILSFQTPPPSAPK--DWVWSGNLCGTPGGEE 250  
Db 295 cglipataytlqicrlwplghwsdpslelrtrteraptvrltdw----- 341  
QY 251 PLLLKAPGPCVQSVKYVFWVGYGRELSPGEGITCCCLIPSGAEWARVSAVNATSWEP-- 308  
Db 342 ----wrq-----rqlprtqlfwkvpbleedsgrlqgy-vvswrpsg 379  
QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335  
Db 380 qagallplcmtelstctfhlpsaeqavalvaynsagtsrtpvfvfesrgpaltrihama 439  
QY 336 ----ELLVTVQPGPGPLEHVVDWARDGPLEKLN--WVRLPPGNLSA-LLPGNFTVGVYP 388  
Db 440 rdphslwvgwepnpwpqgyvlewglgppsasnsnktwmeqngratgflkenirpfql 499  
QY 389 YRITVTAVSASGLASASSVWGFREELAPLVGPTLWRLQDAPGTPAIANGEVPRHQLRGH 448  
Db 500 yeiivtplyqdtmgsqhvayysqemashapel-hlkhigtwaqlewvpeppelgksp 558  
QY 449 LTHYTLCAQSGTSPSVCNMVSGNTQSVTLDPDLPWGPCELW-----VTA 491  
Db 559 lthytifwtanqgsfalsalnassrgfvlhgile--paslyhihlmaasqagatnstvltl 616  
QY 492 STIAGGPGPILRLHLPDNTLRWKVLPGLFLWGLFLL--GCGLSLATSGRCYHLRHK 548  
Db 617 mltltpgs-----elhi-----ilglfllllltclcg----tawlcspnrk 655  
QY 549 VLPRWVWEKVPDPANSSG-----QPHMEQVP--EAQPLGDLPTLEVEEMEP-- 599  
Db 656 ----nplwpsvdpahsigswwptimeedafqlpglgtptlktlvleedekkpvpwesh 711  
QY 600 SOPAQATAPLDSGYEKHFLPTPEELGLL-GPPR 631

Db 712 hnssetcg-----lptlvqyviqgdpr 734

RESULT 15  
AAR11742  
ID AAR11742 standard; Protein: 801 AA.  
XX AAR11742;  
AC AAR11742;  
DT 04-JUL-1991 (first entry)  
DE Clone 25-1 encoded human G-CSF receptor.  
XX granulocyte colony stimulating factor; receptor; clone 25-1.  
KW Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT Peptide 1..24  
FT /label= signal peptide  
FT Protein 25..801  
FT /label= human G-CSFR  
XX  
PN W09105046-A.  
XX  
PD 18-APR-1991.  
XX  
PF 24-SEP-1990; 90WO-0005434.  
XX  
PR 03-APR-1990; 90US-0522952.  
PR 26-SEP-1989; 89US-0412816.  
PR 03-OCT-1989; 89US-0416306.  
XX  
PA (IMMU-) IMMUNEX CORP.  
XX  
PI Smith CA, Larsen AD, Curtis BM;  
XX  
DR WPI; 1991-132853/18.  
DR N-PSDB; AAQ11580.  
XX  
PT Granulocyte-colony-stimulating factor (G-CSF) receptor DNA and  
PT protein - useful as diagnostics and for regulating immune and  
PT inflammatory responses  
XX  
PS Disclosure; Fig 2,3,4,5,6; 34pp; English.  
XX  
CC This is the deduced amino acid sequence of the G-CSFR encoded by  
CC clone 25-1. The C-terminal differs from that encoded by clone D-7  
CC due to an alternative splicing arrangement. The protein can be used  
CC in compositions for use in therapy, diagnosis, assay of G-CSFR, or  
CC in raising antibodies to G-CSFR.  
CC See also AAQ11579.  
XX  
SQ Sequence 801 AA;

Query Match 8.5%; Score 297.5; DB 12; Length 801;  
Best Local Similarity 22.8%; Pred. No. 9e-15;  
Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;  
Qy 50 LNCWEPLGDLGAPSELHLQSQYRSN-KTQTVAV-----AAGRSWAIPREQLTMSDKL 103  
Db 140 llicwepgpethptsftlksfksrgnctgdsildecvpkdgshcciprkhillyqnm 199  
Qy 104 LWV-----GKAGQPLW-----PPVFVNLETQMKPNAPRLG-----PDVDF 139  
Db 200 giwvgaenalgtmspqicldpmdrvklleppmlrtmdpspeaappqagclqlcwep---- 255  
Qy 140 SEDDPLEATVHWAPPTWPSHKVLICQF-HYRRCOEAAWTLLEPELKTIPLPVEIQDLEL 198  
Db 256 -----wqpgllhinqk---celrhkprgeasvalvgp-----lplealgyel 294

Qy 199 -----ATGYKVYGRCRMEKEEDLMGEWSPILSFQPPSAPK---DWVWVSGNLCGTPGGEE 250  
Db 295 cgllpataytlqircirwplpghwsdpslelrtrteraptvrltdw----- 341  
Qy 251 PLLLWKAPGPCVQVSYKYVFWVGGRELSPGEGITCCSLIPSGAEWARYSAVNATSWEP-- 308  
Db 342 ----wrq-----rqlpbrtqlfwkpvpleedsgriqgy-vvswrpsg 379  
Qy 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSISAGST----- 335  
Db 380 qagailplcmttelctfhlpeaqeavalvaynsagtsrptpvfseesrgpaltlhama 439  
Qy 336 ----ELLVTPQPGCEPLEHHVVDWARDGDPLEKLN--WVRLPPGNLSA--LLPGNFTVGV 388  
Db 440 rdphslwgvwepnpwpggyvlewgldgppsasnsnktwrmegngratgflikenirpfql 499  
Qy 389 YRITVTAVSASGLASASSVMGFRRELAPLVGPTLWRLQDAPPCTPAIANGEVPRHQLRGH 448  
Db 500 yeilvtplyqdtmgpsqhvyaysgemapshapel-hlkhgktaqlwlewpvpeppelgksp 558  
Qy 449 LTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLDLPWGPCELW-----VTA 491  
Db 559 lthytfwtwnaqnqsfailnaassrgfvlhgile--paaslyhihlmaasagagatnstvitl 616  
Qy 492 STIAGQGPPGPILRLHLDPDNTLRWKVLPGLFLWGLFL--GCGLSLATSGRCYHLRHK 548  
Db 617 mltltpgs-----elhi-----ilglflllllllclcg-----tawlcspnrk 655  
Qy 549 VLPWRWVEKVPDPANSSSG-----QPHMEQVP--EAQPLGDLPILEVEEMEPPVMES 599  
Db 656 ---nplwpsvdpahsslgswvptimesdafqlpqlgtpttkltvleedekkpvp-wes 711  
Qy 600 SOPAQATAPLDSGYEKHFELPTPEELGLL-GPPR 631  
Db 712 hnssetcg-----lptlvqyviqgdpr 734

Search completed: May 9, 2002, 06:06:12  
Job time: 144 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:03:48 ; Search time 24.01 Seconds  
(without alignments)  
596.089 Million cell updates/sec

Title: US-09-692-504-1

Perfect score: 3498

Sequence: 1 MRGGGAPFWLPLKALL.....FLTPPELGLGPPRPQVLA 636

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	636	1	US-08-653-740-5
2	3498	100.0	636	2	US-09-073-594-5
3	3498	100.0	636	3	US-09-275-925-5
4	3150	90.1	578	1	US-08-653-740-3
5	3150	90.1	578	2	US-09-073-594-3
6	3150	90.1	578	3	US-09-275-925-3
7	2044	58.4	623	1	US-08-653-740-7
8	2044	58.4	623	2	US-09-073-594-7
9	2044	58.4	623	3	US-09-275-925-7
10	380	10.9	862	2	US-08-685-118-2
11	380	10.9	862	2	US-08-915-495-2
12	380	10.9	862	2	US-08-914-520-2
13	298.5	8.5	783	6	5422248-2
14	297.5	8.5	836	1	US-07-923-976-4
15	294.5	8.4	602	2	US-08-419-652-6
16	292	8.3	863	1	US-07-923-976-8
17	277	7.9	837	1	US-07-923-976-2
18	268.5	7.7	771	1	US-07-923-976-6
19	248	7.1	708	1	US-07-797-556-2
20	248	7.1	708	1	US-08-308-881-2
21	248	7.1	708	2	US-09-058-263-2
22	248	7.1	708	2	US-09-059-099-2
23	248	7.1	708	3	US-09-058-264-2
24	248	7.1	708	5	PCT-US95-06530-2
25	247	7.1	918	2	US-08-825-558-6
26	236.5	6.8	572	2	US-08-419-652-5
27	226	6.5	979	1	US-08-308-881-6

28	226	6.5	979	2	US-09-058-263-6	Sequence 6, Appli
29	226	6.5	979	2	US-09-059-099-6	Sequence 6, Appli
30	226	6.5	979	3	US-09-058-264-6	Sequence 6, Appli
31	226	6.5	979	5	PCT-US95-06530-6	Sequence 6, Appli
32	210	6.0	658	2	US-08-825-558-4	Sequence 4, Appli
33	206.5	5.9	1097	1	US-07-943-843-6	Sequence 6, Appli
34	206.5	5.9	1097	1	US-08-347-003-6	Sequence 6, Appli
35	205	5.9	1001	1	US-07-797-556-6	Sequence 6, Appli
36	205	5.9	1001	1	US-07-943-843-2	Sequence 2, Appli
37	205	5.9	1001	1	US-08-347-003-2	Sequence 2, Appli
38	199	5.7	620	2	US-08-419-652-7	Sequence 7, Appli
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40	178	5.1	894	1	US-08-372-892-2	Sequence 2, Appli
41	178	5.1	894	1	US-08-445-640-34	Sequence 34, Appli
42	178	5.1	894	3	US-08-170-558-34	Sequence 34, Appli
43	178	5.1	894	3	US-08-447-314-34	Sequence 34, Appli
44	178	5.1	894	3	US-08-445-461-34	Sequence 34, Appli
45	172	4.9	1711	2	US-08-342-930-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-653-740-5  
; Sequence 5, Application US/08653740  
; Patent No. 5792850  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc. East  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/653,740  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 636 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-653-740-5

Query Match 100.0%; Score 3498; DB 1; Length 636;  
Best Local Similarity 100.0%; Pred. No. 1.7e-280;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGGGAPFWLPLKALLPLLWVLFQTRPQGSAGPLQCYGVGLDNCNWEPLGDL 60  
Db 1 MRGGGAPFWLPLKALLPLLWVLFQTRPQGSAGPLQCYGVGLDNCNWEPLGDL 60

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-073-594-5

Query Match 100.0% Score 3498; DB 2; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.7e-280;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 NLGCTPGGEEPLLWKAPGCVQVSYKVFVWVGGRLESPGEGITCCCSLIPSGAEWARVSA 300
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Db 301 VNATSWEPITNLSVCLDSASAPRSVAVSSIAGSTELLVWQPGPELEHVVDWARDGD 360
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RESULT 3
US-09-275-925-5
; Sequence 5, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESS: ZymoGenetics, Inc.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,594
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-073-594-5

Query Match 100.0% Score 3498; DB 2; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.7e-280;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGGGAPFWLWPLPKALLPLLLWLFQTRPQGSAGPLQCYGVGGLDNLNCSWEPLGDL 60
Db 1 MRGGGAPFWLWPLPKALLPLLLWLFQTRPQGSAGPLQCYGVGGLDNLNCSWEPLGDL 60
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Db 61 GAPSELHLQSKYRSNKTOTVAAAGRSWVAIPREQLTMSDKLLVWGTAKAGQPLWPPVFV 120
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Db 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHMAPTWPSHKVLICQPHYRRCQEAATLLE 180
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Db 241 NLGCTPGGEEPLLWKAPGCVQVSYKVFVWVGGRLESPGEGITCCCSLIPSGAEWARVSA 300
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Db 301 VNATSWEPITNLSVCLDSASAPRSVAVSSIAGSTELLVWQPGPELEHVVDWARDGD 360
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Db 541 RCYHLRHKVLPKRWVWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWESS 600
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RESULT 3
US-09-275-925-5
; Sequence 5, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
```



ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-31  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 636 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-275-925-5

Query Match 100.0%; Score 3498; DB 3; Length 636;  
Best Local Similarity 100.0%; Pred. No. 1.7e-280;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGRGAPFWLWPLPKLALLPVLVLFQTRPQGSAGPLQCYGVGVLGDLNCSWEPLGDL 60  
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Qy 361 PLEKLNWVRLPPGNLSALLPQNFVGVYRITVAVSAGSLASSVWGFREELAPLVGP 420  
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Qy 421 TLWRLODAPPGTATANGVEPRHQLRHLTHYTICAQSGTSPVCMVSGNTQSVTLDPDL 480  
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Db 481 PWGCELVWVTAATAGQCPGPIRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540  
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Db 541 RCYHLRHKVLPWWKEVDPANSSGQPHMEQVPEAQPLGDLPILEYEEMEPVPMESS 600

Db 541 RCYHLRHKVLPWWKEVDPANSSGQPHMEQVPEAQPLGDLPILEYEEMEPVPMESS 600  
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Db 601 QPAQATAPLDSGYEKHFLPTPEELGLLGP RPQVLA 636  
RESULT 4  
US-08-653-740-3  
Sequence 3, Application US/08653740  
Patent No. 5792850  
GENERAL INFORMATION:  
APPLICANT: James W. Baumgartner  
APPLICANT: Donald C. Foster  
APPLICANT: Frank J. Grant  
APPLICANT: Cindy A. Sprecher  
TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-31  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 578 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-653-740-3

Query Match 90.1%; Score 3150; DB 1; Length 578;  
Best Local Similarity 90.9%; Pred. No. 7.7e-252;  
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

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Db 1 MRGRGAPFWLWPLPKLALLPVLVLFQTRPQGSAGPLQCYGVGVLGDLNCSWEPLGDL 60  
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Db 61 GAPSELHQSQRYSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPPV 120  
Qy 121 NLETQMKNPAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCQEAATLLE 180  
Db 121 NLETQMKNPAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCQEAATLLE 180  
Qy 181 PELKTIPTVPIQDELEATGYKVYGRRCMEKEEDLWGEWSPILSFQTPPSAPKDVVWSG 240  
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Db 241 NLCGTPGGEPLLLWKAAPGVQVSYKVFVWVGRELSPEGITCCSLIPSGAEWARVSA 300

QY 301 VNATSWPLTNLSVCLDSASAPRSVAVSSIAGSTELLVTWQPGCEPLEHHVVDWARDGD 360  
DB 301 VNATSWPLTNLSVCLDSASAPRSVAVSSIAGSTELLVTWQPGCEPLEHHVVDWARDGD 360  
QY 361 PLEKLNWRLPPGNLSALLPGNFTVGVYRITVTAVSASGLASSVWGFREELAPLVGP 420  
DB 361 PLEKLNWRLPPGNLSALLPGNFTVGVYRITVTAVSASGLASSVWGFREELAPLVGP 420  
QY 421 TLWRLQDAPPGTPTAIAMGEVPRHQLRGHLTHYTLCAQSGTSPSCVMNVSNTQSVTLPLDL 480  
DB 421 TLWRLQDAPPGTPTAIAMGEVPRHQLRGHLTHYTLCAQSGTSPSCVMNVSNTQSVTLPLDL 480  
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DB 481 PWGPCELWVTASTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLLGCGLSLATSG 540  
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DB 601 QPAQATAPLDSGYEKHFLPTPELGLGPPRPQVLA 636  
QY 567 -----GLLGPPRPQVLA 578  
DB 567 -----GLLGPPRPQVLA 578

RESULT 5  
US-09-073-594-3  
; Sequence 3, Application US/09073594  
; Patent No. 5925735  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,594  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 578 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-073-594-3

Query Match 90.1%; Score 3150; DB 2; Length 578;  
Best Local Similarity 90.9%; Pred. No. 7.7e-252;  
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

QY 1 MRGGRGAPFWLWPLPKLALLPLLWVLFQRTPOGSAGPLQCYGVGDLGDLNCSWEPLGDL 60  
DB 1 MRGGRGAPFWLWPLPKLALLPLLWVLFQRTPOGSAGPLQCYGVGDLGDLNCSWEPLGDL 60  
QY 61 GAPSELHLQSQKVRSNKTOQVAAAGRSWVAIPREQLTMSDKLLVMGTAKAGQPLWPPVFV 120  
DB 61 GAPSELHLQSQKVRSNKTOQVAAAGRSWVAIPREQLTMSDKLLVMGTAKAGQPLWPPVFV 120  
QY 121 NLEQTKMPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCQEAATLLE 180  
DB 121 NLEQTKMPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCQEAATLLE 180  
QY 181 PELKTIPLTPVETQDLELATGYKYVGRCKMEKEEDLWGEWSPILSQTTPPSAPKDVWVSG 240  
DB 181 PELKTIPLTPVETQDLELATGYKYVGRCKMEKEEDLWGEWSPILSQTTPPSAPKDVWVSG 240  
QY 241 NLGCTPGGEEPLLLWKAPGCVQVSYKVMFWVGRELSPGITCCCSLIPSGAEWARVSA 300  
DB 241 NLGCTPGGEEPLLLWKAPGCVQVSYKVMFWVGRELSPGITCCCSLIPSGAEWARVSA 300  
QY 301 VNATSWPLTNLSVCLDSASAPRSVAVSSIAGSTELLVTWQPGCEPLEHHVVDWARDGD 360  
DB 301 VNATSWPLTNLSVCLDSASAPRSVAVSSIAGSTELLVTWQPGCEPLEHHVVDWARDGD 360  
QY 361 PLEKLNWRLPPGNLSALLPGNFTVGVYRITVTAVSASGLASSVWGFREELAPLVGP 420  
DB 361 PLEKLNWRLPPGNLSALLPGNFTVGVYRITVTAVSASGLASSVWGFREELAPLVGP 420  
QY 421 TLWRLQDAPPGTPTAIAMGEVPRHQLRGHLTHYTLCAQSGTSPSCVMNVSNTQSVTLPLDL 480  
DB 421 TLWRLQDAPPGTPTAIAMGEVPRHQLRGHLTHYTLCAQSGTSPSCVMNVSNTQSVTLPLDL 480  
QY 481 PWGPCELWVTASTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLLGCGLSLATSG 540  
DB 481 PWGPCELWVTASTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLLGCGLSLATSG 540  
QY 541 RCYHLRHKVLPKRWWEKVPDPANSSSQPHMEQVPEAQPLGDLPLILEVEEMEPFVWESS 600  
DB 541 RCYHLRHKVLPKRWWEKVPDPANSSSQPHMEQVPEAQPLGDLPLILEVEEMEPFVWESS 600  
QY 601 QPAQATAPLDSGYEKHFLPTPELGLGPPRPQVLA 636  
DB 601 QPAQATAPLDSGYEKHFLPTPELGLGPPRPQVLA 636  
QY 567 -----GLLGPPRPQVLA 578  
DB 567 -----GLLGPPRPQVLA 578

RESULT 6  
US-09-275-925-3  
; Sequence 3, Application US/09275925  
; Patent No. 6080406  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/275,925  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:

NAME: Parker, Gary E  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 578 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-275-925-3

Query Match 90.1%; Score 3150; DB 3; Length 578;  
Best Local Similarity 90.9%; Pred. No. 7.7e-252;  
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;  
Qy 1 MRGGRGAFWLPKLLALLVLFQTRPQSGAGPLQCYGVGPGDLNCSWEPLGDL 60  
Db 1 MRGGRGAFWLPKLLALLVLFQTRPQSGAGPLQCYGVGPGDLNCSWEPLGDL 60  
Qy 61 GAPSELHLSQKYSRKNKTQTAVAAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPPPVFV 120  
Db 61 GAPSELHLSQKYSRKNKTQTAVAAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPPPVFV 120  
Qy 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPTPWPSHKVLICOFHYRRCOEAAWTLLE 180  
Db 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPTPWPSHKVLICOFHYRRCOEAAWTLLE 180  
Qy 181 PELKTIPTVPIQDLATGYKYVGRCRMKEEDLWSEWSPILSFQTPPSAPKDVWVSG 240  
Db 181 PELKTIPTVPIQDLATGYKYVGRCRMKEEDLWSEWSPILSFQTPPSAPKDVWVSG 240  
Qy 241 NLCTPGGEEPLLLWKAPCPQVSYKVFVWGGRELSPEGITCCSLIPSGAEWARVSA 300  
Db 241 NLCTPGGEEPLLLWKAPCPQVSYKVFVWGGRELSPEGITCCSLIPSGAEWARVSA 300  
Qy 301 VNATSWEPDLNLSLVCLDSASAPRSVAVSSVWGGRELSPEGITCCSLIPSGAEWARVSA 360  
Db 301 VNATSWEPDLNLSLVCLDSASAPRSVAVSSVWGGRELSPEGITCCSLIPSGAEWARVSA 360  
Qy 361 PLEKLNWVRLPPGNLSALLPQNTVGVYRITVTAVASGLASASVWGFREELAPLVGP 420  
Db 361 PLEKLNWVRLPPGNLSALLPQNTVGVYRITVTAVASGLASASVWGFREELAPLVGP 420  
Qy 421 TLWRLODAPPGTATAMGEVPRHQLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLD 480  
Db 421 TLWRLODAPPGTATAMGEVPRHQLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLD 480  
Qy 481 PWGPCELVWTTASTIAGQPPGPILRLHLPDNTLRKVLPGILFLWGLFLGCGLSLATSG 540  
Db 481 PWGPCELVWTTASTIAGQPPGPILRLHLPDNTLRKVLPGILFLWGLFLGCGLSLATSG 540  
Qy 541 RCYHLRHKVLRVWKEVDPDANSSSGQPHMEQVPEAQLDGLPILVEEEMEPVPMESS 600  
Db 541 RCYHLRHKVLRVWKEVDPDANSSSGQPHMEQVPEAQLDGLPILVEEEMEPVPMESS 600  
Qy 601 QPAQATAPLDSYKHEKFLPTPEELGLGPPRPQVLA 636  
Db 567 -----GLLGP RPQVLA 578

RESULT 7  
US-08-653-740-7  
Sequence 7, Application US/08653740  
Patent No. 5792850  
GENERAL INFORMATION:  
APPLICANT: James W. Baumgartner  
APPLICANT: Donald C. Foster  
APPLICANT: Frank J. Grant  
APPLICANT: Cindy A. Sprecher

TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/653,740  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 623 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-653-740-7

Query Match 58.4%; Score 2044; DB 1; Length 623;  
Best Local Similarity 62.8%; Pred. No. 1.7e-160;  
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy 14 LPKALLPLLWLFQTRPQSGAGPLQCYGVGPGDLNCSWEPLGDLGAPSELRLQSQKY 73  
Db 9 LTPLELLLSLMLGTRPHGSPGLQCYGVGPGDLNCSWEPLGDLGAPSELRLQSQKY 68  
Qy 74 RSNKQTQVAAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPPPVVNLTKMKNAPRL 133  
Db 69 HFNRVMEVVPKQSWVTIPREQFTMADKLLMGTKGRPLWSSVSVNLETKMKNAPRL 128  
Qy 134 GPDVDFSEDDPLEATVHWAPTPWPSHKVLICOFHYRRCOEAAWTLLEPELKTPLTPVEI 193  
Db 129 FSQVDISEATLEATVQWAPPVWPPKALTCQFHYRRCOEAAWTLLEPELKTPLTPVEI 188  
Qy 194 QDLLEATGYKYVGRCRMKEEDLWSEWSPILSFQTPPSAPKDVWVWGGRELSPEGITCCSLIPSGAEWARVSAVWGFREELAPLVGP 253  
Db 189 QNLPTCTCYQVSGRCQVNGYP-WGEMSSPLSFQTPFLDPEDVWVWGGRELSPEGITCCSLIPSGAEWARVSAVWGFREELAPLVGP 247  
Qy 254 LKAKGPCVQVSYKVFVWGGRELSPEGITCCSLIPSGAEWARVSAVWGFREELAPLVGP 313  
Db 248 VNKDPRPCQVYTYVWFGAGDITTTQEEVPCCKSPVPAWMEVAVVSGNSTSWVPPTNLS 307  
Qy 314 LVCLDSASAPRSVAVSSVWGGRELSPEGITCCSLIPSGAEWARVSAVWGFREELAPLVGP 373  
Db 308 LVCLAPESAPCDVGVSSADGSPGKVTWKQGTGTRKPLEYVVDNAQDGSLOKLNWTLRPPG 367  
Qy 374 NLSALLPGNFTVGVYRITVTAVASGLASASVWGFREELAPLVGP 433  
Db 368 NLSALLPGNFTVGVYRITVTAVASGLASASVWGFREELAPLVGP 427  
Qy 434 ATAMGEVPRHQLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLD 493  
Db 428 VVAMGEVPRHQLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLD 487  
Qy 494 IAGQPPGPILRLHLPDNTLRKVLPGILFLWGLFLGCGLSLATSG 549  
Db 488 VAGQPPGPILRLHLPDNTLRKVLPGILFLWGLFLGCGLSLATSG 547

Qy	14	LPKLLALLPLWLVL	QRTTRPOGSGACPLQCGV	GPLDNLCSWEPLGDLGAPSELHUSQKY	73
Db	9	LTPLELLLSLMSLLG	TRPHGSPCLQCGV	GPLGLTNGSWEPLGDLTPPVLYHQSQKY	68
Qy		RSNKTOTVAAGRSWA	IPREGILTMSDKLLV	MGTKAGOLPWPVFNLETKMKNAPRL	133
Db	69	HPARVNEVKVP	SKQSWTIPREQFTWADKLLI	MGTKOGRPLWSSVFNLETKMKNPTPQI	128
Qy	134	GPVDVDFSEDDPLEAT	VHAPPTWPSHKVLICQ	PHYRRCEAAWTLLEPELKTIPITPVEI	193
Db	129	FSQVDISEEATLEAT	VQWAPPVPPQKALTC	QFRYKECQAEAWTRLEPQLKTDGLTPVEM	188
Qy	194	QDLELATGKYVGR	CRMEKEEDLWGSNPIL	SFQTPPSAPKQVWVSGNLCGTPPGGEPLL	253
Db	189	QNELEPGTCYVGR	CGRCVNGYGP-WG	SWSSPLSFQTPFLDPEWVSGTVCESGKRAALL	247

```

RESULT          9
US-09-275-925-7
; Sequence 7, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/275,925
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-275-925-7

```

Query Match	Score 2044;	DB 3;	Length 623;
58.48;	Score 2044;	DB 3;	Length 623;

Best Local Similarity 62.8%; Pred. No. 1.7e-160;  
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy 14 LPKALLLWLFORTPOGSAQCYGPGGLDNLCSWEPLGDLGAPSELHQSOQY 73  
Db 9 LTPLELLSLMLLGTGRPHSGPGQCYGPGGLILCSWEPLGDLTPPVLYHQSOQY 68

Qy 74 RSNKTQTVAVAGRSWAIPREQLTMSDKLLVMGTAKQOPLWPPVFVNMKPNAPRL 133  
Db 69 HPNRVWEVKVPSKQSWVTPREQLTMDKLLWGTQKRLWSSVSNLETKMTPQI 128

Qy 134 GPDVDFSEDDPLEATVHWAPTWESHKVLICOFHYRRCQEAATLLELKTPIPTVEI 193  
Db 129 FSQVDISEATVQWAPWPPQKALTQFRYKCEQAEATWLEPOLKTDGLTPVEM 188

Qy 194 QDLELATGYKVGRCRMEKEEDLWEMSPILSFQTPPSAPKDVVYSGNLGCTPGGEEPL 253  
Db 189 QNLEPGTCYQVSGRCOVENGYP-NGEWSPLSFQTPFLDPEDVWVSGIVCTSGKRAALL 247

Qy 254 LKAPGPCVQVYKVFVWGGRELSPEGITCCSLIPSGAEWARVSNATSWEPNLNLS 313  
Db 248 VMKDPKPCQVYTYVMFGAGDITTTQEEVPCCKSPVPAWMEWAVVSPGNSTSWVPPTNLS 307

Qy 314 LVCILDSASAPRSVAVSTAGSTELLVWQPGPGRPLEHVDVWDGDPLEKLNWVRLPPG 373  
Db 308 LVCLAPESAPCDGVSSADSGPGIKVWTKQGRKPLFVVDWAQDGSIDLKLNWTRLP 367

Qy 374 NLSALLPFGNTVGPYRITVAVASGLASASSVMGFEEELAPLVGPTLWRLQDAPPGTP 433  
Db 368 NLSLLPGEKFGVPYRITVAVYSGGLAAAPSVMGFEEELVPLAGPAVWRLPDDPGCTP 427

Qy 434 AIANGEVPRHQLRHLHYTHYTCAGSGTSPSCMVNMGNTQSVTLPDLPWGCELMVWAST 493  
Db 428 VVANGEVPRHQLRHLHYTHYTCAGSGTSPSCMVNMGNTQSVTLPDLPWGCELMVWAST 487

Qy 494 IAGOGPGPILRLPDLNTRKWLPGTLFLWGLFLGCGLSLATS-----GRCVHLRKY 549  
Db 488 VAGOGPGPILRLPDLNTRKWLPGTLFLWGLFLGCGLSLATS-----GRCVHLRKY 547

Qy 550 LPRVWEKVPDPANSSQHPHMEQVPEAQPLGDLPILEVEEMEPVPMVSSQPAQATPL 609  
Db 548 LPQWIERVDPANSSQHPHMEQVPEAQPLGDLPILEVEEMEPVPMVSSQPAQATPL 604

Qy 610 DSGYEKHLPTPEELGLL 627  
Db 605 YSGYEKHLPTPEELGLL 622

FIG. 10  
us-09-692-504-1-rai  
Sequence 2, Application US/08685118  
Patent No. 5840530  
GENERAL INFORMATION:  
APPLICANT: Gubler, Ulrich A  
APPLICANT: Presky, David H  
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: NJ  
COUNTRY: USA  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,118  
FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Silverman, Robert A.  
REGISTRATION NUMBER: 35,682  
REFERENCE/DOCKET NUMBER: CD 9195  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-2863  
TELEFAX: (201) 235-2363  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 862 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-685-118-2

Query Match 10.9%; Score 380; DB 2; Length 862;  
Best Local Similarity 25.3%; Pred. No. 6.2e-23;  
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

Qy 31 RPOGSAGPLQCYGPGGLDNLCSWEPLGDLGAPSELHQSOQY-----LGAPSELHQSOQY----- 71  
Db 126 QPQN-----LSCIQKGEQGTACTWGERGRDTHLYTEYLQLSGPKNLTWQCKQDIYCDYL 181

Qy 72 -----KYRSNKTQTV-AVAGRSWAIPREQLTMSDKLLVMGTAKQOPLWPPVFVNM 121  
Db 182 DFGILNTPESPESNFTAKVTAVNSLGSSSSLP-STFTFLDIV-----RPL-PPWDIR 231

Qy 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHWAPTWESHKVLICOFHYRRCQEAATLLEP 181  
Db 232 IKFQ-KASVSR-----CTLYWR-----DEGLVLLNRLRYRSPNSRLNWN----- 269

Qy 182 ELKTIPLFPV-----ETQDLELATGYKVGRCRMEKEEDLWEMSPILSFQTP-----PSAPK 234  
Db 270 ----VNVTKAKGRHLLDLKPTFEYEFQISSLHLKLYKSGSDWSESLRAQTPPEEPTGML 325

Qy 235 DVWVSGNLGCTPGGEEPLLLWK-----APGPCVQVYKVFVWGGRELSPE--GITCCC 286  
Db 326 DVVYMKRHIDY-SRQQISLFWKNLSVSEARGKILHYQVTLQELTGKAMTQNTGHTSWT 384

Qy 287 SLIPSGAEWA-RVSAVNA--TSWEPLTNLSLVCILDSASAPRSVAVSSVSIAGSTELLVWTP 343  
Db 385 TVIPTGHWAVAVSAANSKGSLSLPTRNINMICEAGLLAPQVSAANS-EGMDNILLVWTP 443

Qy 344 ---GPGEPLHVVWDWAR---DGDPLEKLNWRLPPLNCSALLPGNFTVGPYRITVAVS 397  
Db 444 PRKDPQSAVQEVVVENRELHPGCDTQVPLNWLRSRPVNSALISENIKSYICYEIRVYALS 503

Qy 398 ASGLASASSVMGFEEELAPLVGPTLWRLQDAPPGTPAIANGEVPRHQLRHLHYTHYTL 455  
Db 504 GD-QGGCSSILGNSKHKAPLSGPHINAITE-EKGSILISWNSIPVQEQMGCLLHYRIYWK 561

Qy 456 -AQSGTSPSVC---MNVSGNTQSVTLPDLPWGCELMVWASTIAGGPPGPILRLHLPDN 511  
Db 562 ERDSNQFQICEIPYRVSONSHIPNSLQ-PRVYVYLMWLTALTAAGESSHGNREPCCL-OG 619

Qy 512 TLRWK--VLPGLI---LFLWGLFLGCGLSLATSGRGYHLRHLRVL-----PRWWEKVP 559  
Db 620 KANWMAFVAPSTICIAIMVGIF-----STHYFQKQVFLVLAALRQWCSREIP 667

Qy 560 DPANSSSQPH-----MEQVPEAQPLGDLPILEVEEMEPVPMVSSQPAQATA-----PLD 610  
Db 668 DPANSTCAKYPVIAEKTQLPLDRLLIDWPTPE---DPEPLVSEVLHQVTPVFRHPPC 723

Qy 611 SCYEKHLPTPEELGLL-----PPRQVPL 635  
Db 724 SNWPO-----REKGIQGHQASEKDMHMSASSPPPPRAL 756

RESULT 11  
US-08-915-495-2  
Sequence 2, Application US/08915495  
Patent No. 5852176

;; GENERAL INFORMATION:  
;; APPLICANT: Gubler, Ulrich A  
;; APPLICANT: Presky, David H  
;; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Hoffmann-La Roche Inc.  
;; STREET: 340 Kingsland Street  
;; CITY: Nutley  
;; STATE: NJ  
;; COUNTRY: USA  
;; ZIP: 07110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/915,495  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/685,118  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Silverman, Robert A.  
;; REGISTRATION NUMBER: 35,682  
;; REFERENCE/DOCKET NUMBER: CD 9195  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (201) 235-2863  
;; TELEFAX: (201) 235-2363  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 862 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-915-495-2

Query Match 10.9%; Score 380; DB 2; Length 862;  
Best Local Similarity 25.3%; Pred. No. 6.2e-23;  
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGSAGPLQCYGVGPGDLNCSWEPLGD-----LGAPSELHLQSQ----- 71  
Db 126 QPQN-----LSCIQKGQGVACTWGRGTRTHLYTEYTLQSLGPKNTWQCKDIYCDYL 181  
QY 72 -----KYRSNKTQTV-AVAAGRSWVAIPREQLTMSDKLLVWCTKAGQPLWPPFVN 121  
Db 182 DFCINLTSPESPENFTAKVTAVNSLGSLSLP-STFTFLDIV-----RPL-PPWDIR 231  
QY 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHVAPPTWPSHKVLICQFHYRCQEAATLLLEP 181  
Db 232 IKFQ-KASVSR-----CTLWVR-----DEGLVLLNRLRYRPSNRLNMN----- 269  
QY 182 ELKTIPTLV-----ETQDLELATGYVYCKRKEKEDLWGEWSPILSFOTP---PSAPK 234  
Db 270 -----VNVTKAKGRHLLDLKPTEYEFQISSKLHLKGSWDSLSRAQTPEEPTGML 325  
QY 235 DVWVSNLCGTGGEPLLLWK-----APGPCVQVSYKVFVWGVGRELSP-EGITCC 286  
Db 326 DVWYMKRHIDY-SRQGISLFWKNLSVSEARGKILHYQVTLQELTGCKAMTQNTIGHTSWT 384  
QY 287 SLIPSGAENA-RVSAVNA--TSWEPLTNLSLCLDSASAPRSVAVSSVSSAGSTELLVTWOP 343  
Db 385 TWIPTGNWAVASANSKSSSLPTRINTMNLCEAGLLAPRQVSANS-ECMDNILVTWOP 443  
QY 344 ---GQCEPLEHVVDWAR---DGDPLEKLNWRLPPGNLSALLPGNFTVGPVYRITVTAVS 397  
Db 444 PKDPSAVQEVVVEHRELHPGGDTQVPLNWLRSRPNVNSALLSENKSYICVIRYALS 503  
QY 398 ASGLASASSWVGFEELAPLVGPTLWRLQDAPPGTPTAIWGEVPRHLRGHLTHYTLCL- 455

Db 504 GD-QGCCSSILGNSKHKAPLSGPHINAITE-EKGSILISWNSIPVQEQMGCLLHYIYWK 561  
QY 456 -AQSGTSPSVC---MNVSGNTQSVTLPLDLPWGCELVWVTASTIAGOGPPGPIRLRLHPDN 511  
Db 562 ERDSNSQPQLCEIPYRVSONSHPINSLQ-PRVTYVLMWTALTAAAGSSHGNEREFCL-QG 619  
QY 512 TLRWK--VLPGI---LFLWGLFLLGGLSLATSGRCYHLRHKVL-----PRWVWEKVP 559  
Db 620 KANWMAFVAPSICTAIIMVGIF-----STHYFOQKVFLVLLAALRPQWCSREIP 667  
QY 560 DPANSSGQPH-----MEQVPEAQPLGDLPILEVEEMEPVPPVMESSQPAQATA-----PLD 610  
Db 668 DPANSTCAKKYPTAEKTLQPLDLLIDWPTPE---DPEPLVISEVLHVQTVFVRHPPC 723  
QY 611 SGYKHFLLTPPELGLLG-----PPRPQVL 635  
Db 724 SNWPQ-----REKGIQGHQASEKMMHSSASSPPPPRAL 756  
RESULT 12  
US-08-914-520-2  
; Sequence 2, Application US/08914520  
; Patent No. 5919903  
; GENERAL INFORMATION:  
; APPLICANT: Gubler, Ulrich A  
; APPLICANT: Presky, David H  
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/914,520  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/685,118  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silverman, Robert A.  
; REGISTRATION NUMBER: 35,682  
; REFERENCE/DOCKET NUMBER: CD 9195  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201) 235-2863  
; TELEFAX: (201) 235-2363  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 862 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-914-520-2

Query Match 10.9%; Score 380; DB 2; Length 862;  
Best Local Similarity 25.3%; Pred. No. 6.2e-23;  
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGSAGPLQCYGVGPGDLNCSWEPLGD-----LGAPSELHLQSQ----- 71  
Db 126 QPQN-----LSCIQKGQGVACTWGRGTRTHLYTEYTLQSLGPKNTWQCKDIYCDYL 181  
QY 72 -----KYRSNKTQTV-AVAAGRSWVAIPREQLTMSDKLLVWCTKAGQPLWPPFVN 121

```
Db 182 DFGINTPESPENFTAKVTAVNSLGSSSLP-STFTFLDIV-----RPL-PPWDIR 231
Qy 122 LETOMKPNAPRLGPDVDESDPLATVHWAPPTWPSHKVLICQPHYRCQEAANTLLEP 181
Db 232 IKFO-KASVR-----CTLYWR-----DEGLVLLNRLRYRPSNRLNM--- 269
Qy 182 ELKTIPLTPV---BIQDELEATGYKVGRCRMEKEEDLWGSPILSFQTP---PSAPK 234
Db 270 ----VNVTKAKGRHLLDKPTEYEFQISKLHLKGSWSWSLSRAQTPPEEPTGML 325
Qy 235 DVMWVSGNLCGPGGEPILLMK-----APGCVQVSKVFWVWGGRELSPE--GITCCC 286
Db 336 DVMWVWKRHDY--SRQISLFWKNLSVSEARGKILHYQVTLQELTGKAMTQNTIGHTSWT 384
Qy 287 SLIPSGAEMA-RVSAVNA--TSWEPLTNLSLVCDSASAPRSVAVSSVSTAGSTELLVWQ 343
Db 395 TVIPRTGNWAVASANKGSLPTRINIMNLCEAGLLAPROVSANS-EGMDNILVWQ 443
Qy 344 ---GGEPELHVVDWAR---DGDPLEKLNWVRLPPGNLSALLPGNFTVGVYRITVAVS 397
Db 444 PRKDSAVQEVVVENRELHPGDTQVPLNWLRSRPNVNSALISENIKSVICVEIRYALS 503
Qy 398 ASGLASASVWCFRELAPLVPPTLWRQDAPPGTAPATANGVPRHQLRHLYTHLTC-- 455
Db 504 GD-QGCSILGNSHKAPLSPGHINAITE-EKGSILISWNSIPVQEQMGCCLLHYRYWK 561
Qy 456 -AQGSTSPVC---MNVSGTQSVTLPLDLPWGPCBLWVTAAGPGPPGPIRLHLDPN 511
Db 562 ERDSNSQOLCEIPRVSONSHINSLO-PRVYVLMWLTALTAAGSSHGNERECL-QG 619
Qy 512 TLRWK--VLPGI---LFLWGLFLCCGLSLATSGRCYHLRHKVL-----PRWYMEKVP 559
Db 620 KANMAFAPSICIAIIMVGIF-----STHYFOQKVFVLLAALRPQWCSREIP 667
Qy 560 DPANSSSQPH-----MEQVPEAQPLDLPLEVEEMEPVWESSQPAQATA-----PLD 610
Db 668 DPANSTCAKPYPIAEKTLPLDLRLIDWPTPE-----DPELVISEVLHQVTPVFRHPPC 723
Qy 611 SOYEKHFLLPTEELGLG-----PPRPQVL 635
Db 724 SNWPQ-----REKGIQHQASEKDMHMSASSPPPPRAL 756

RESULT 13
5422248-2
; APPLICANT: SMITH, CRAIG A.; LARSEN, ALF D.; SIMS, JOHN E.;
; INVENTOR: CURTIS M.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING GRANULOCYTE-COLONY
; STIMULATING FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/6,183
; FILING DATE: 13-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 587,329
; FILING DATE: 24-SEP-1990
; APPLICATION NUMBER: 522,952
; FILING DATE: 03-APR-1990
; APPLICATION NUMBER: 416,306
; FILING DATE: 03-OCT-1989
; APPLICATION NUMBER: 412,816
; FILING DATE: 26-SEP-1989
; SEQ ID NO.: 2
; LENGTH: 783
5422248-2
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Query Match 8.5%; Score 298.5; DB 6; Length 783;
Best Local Similarity 22.5%; Pred. No. 2.9e-16;
Matches 160; Conservative 75; Mismatches 250; Indels 227; Gaps 34;
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Qy 50 LNCMSPEPLDGLGAPSELHQSQYRSN-KTQTVAV-----AAGRSWVAIPREOLTHSDKL 103
Db 140 LICOWEPGPEETHLPTSTFKSFGRCNGCOTQDSDILDCVPKDGQSHCCIPRKHLLEYQNM 199
Qy 104 LVN-----GFKAGQPLW-----PPVFVNLETKMKNAPRLG-----PDVDF 139
Db 200 GIWVOAENALGTSMSQCLCDPMDVVVKLEPPMLRTMDPSPEAAPQAGCQLCWEP--- 255
Qy 140 SEDDPLEATVHWAPPTWPSHKVLICQF-HYRCQEAANTLLEPELKTIPLTPEIQLDEL 198
Db 256 -----WQPGHLINQK---CELRLKQGEASWALVGP-----LPLEALQYEL 294
Qy 199 -----ATGYKVGRCRMEKEEDLWGSPILSFQTPPSAPK---DVMWVSGNLCGTPGEE 250
Db 295 CGLLPATATVTLQIRCNWPLPGHWSWDSLSLELRTERRAPTVRDLTW----- 341
Qy 251 PLLLWKAPCPQVQVSKVFWVWGGRELSPEGITCCSLIPSGAEWARVSAVNATSHEP-- 308
Db 342 ---WRQ-----RQDPRTVOLFVKWPKVPLEEDSGRIQGY-VVSWRPSG 379
Qy 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSVSIAGST----- 335
Db 380 QAGAILPLCNTTTELSCTFHLPSAEQVALVAYNSAGTSRPTPVVFSERGPALTRLHAMA 439
Qy 336 -----ELLVWQPGCEPLEHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGP 388
Db 440 RDPHSLWGWEPNPMWPGYVIEWGLGPPSASNSKNTWRMEQNGRATGFLKENIRPFOL 499
Qy 389 YRITVAVSASGLASASSVWGFEELAPLVGPTLWRQDAPPGTAPATANGVPRHQLRGH 448
Db 500 YEIIVTPLYQDTMGPSQHVYAYSOEMAPSHAPEL-HLKHIGKTAQWLEWVPEPELKGSP 558
Qy 449 LTHYTLCAQSGTSPSCVMNVSGTQSVTLPLDLPWGPCBLW-----VTA 491
Db 559 LTHYTLFWTNAQNSFSAITLNASSRGFVLHGLE--PASLYHIHLMAASQAGATNSVTLT 616
Qy 492 STIAGQGGPPIRLHLPDNTLRKWLPGILFIMWGLFLL---GCGLSLATSGRCYHLRHK 548
Db 617 MTLTPEGS-----ELHI-----ILGLFGLLLLTCLCG---TAWLCCSPNRK 655
Qy 549 VLPWVWEKVPDPANSSSG-----QPHMEQVP--EAQPLDLPLEVEEMEPVWESSQPAQATAP-LDSGYEKHFLLPTEELGLLGP 631
Db 656 ---NPLWSPVDPFAHSSLSGWSVPTIMEEDAFQLPGTPTTKLTVLEDEKKPVWESH 712
Qy 596 -----VWESSQPAQATAP-LDSGYEKHFLLPTEELGLLGP 631
Db 713 NSSETCGLPTLVQTVYVLQGDPRAVSTQPOSQSG-----TSQD---AGP 754

RESULT 14
US-07-923-976-4
; Sequence 4, Application US/07923976
; Patent No. 5574136
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigekazu
; APPLICANT: Fukunaga, Rikio
; TITLE OF INVENTION: DNA Encoding Granulocyte
; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones, Tullar & Cooper, P.C.
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,976
; FILING DATE: 19920922
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74539/1990
; FILING DATE: 23-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 176629/1990
; FILING DATE: 03-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP91/00375
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hellwege, James W.
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 514853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-415-1500
; TELEFAX: 703-415-1508
; INFORMATION FOR SEQ ID NO: 4:
; LENGTH: 836 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-923-976-4

Query Match      8.5%; Score 297.5; DB 1; Length 836;
Best Local Similarity 22.8%; Pred. No. 3.8e-16;
Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;

QY 50 LNCSEPLDGLGAPSELHLQSKYRSN-KTQTVAV-----AAGRSWAIPREOLTHMSDKL 103
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 140 LICQWEPGPGTHLPTFTLKSKFSGRCNCQTQGSILDCVPKQGSCHCCIPRKHLLYQNM 199
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 104 LVW-----GKAGQPLW-----PPVEVNLETKMKNAPRLG-----PDVDF 139
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 200 GIWVQAEALGTSMSPOLCLDPMVYKLEPPMLRTWDPSPEAAPQAGCLQLCWEP--- 255
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 140 SEDDPLEATVHMAPTPWPSHKVLICQF-HYRRCQEAANTLLEPELKTPIPTPVEIQDLEL 198
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 256 -----WQGLHINQ-----CELRHKPQGEASWALVG-----LPLEALQYEL 294
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 199 -----ATGKYVGRCRMEKEEDLWGEWSPILSPQTTPPSAPK-----DWMVSGNLCGTPGGEE 250
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 295 CGLLPATAYTLQIRCIWPLCPHWSWSPSLRLTTERAPTVRLDTW----- 341
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 251 PLLLWAPGPGCVQVSKYVFWVGGRGELSPGTCCLSLIPSGAEWARSVAVNATSWEP-- 308
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 342 ----WQ-----RQDPTVOLFWKVPLEEDSGRIQGY-VVSWRPSG 379
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 380 QAGAILPLCNTTSLCTFHLPSAEQVALVAYNSAGTSRPTPVFSESGRPALTRLHAMA 439
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 336 -----ELLVTWQPGPGPLEHVVDWARDGDPLEKLN--WYRLPPGNLSA--LLPGNFTVGV 388
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 440 RDPHSLWVGWEPNPWPGQVYVIEWGLGPPSPASNSNKTWRMEQNGRATGFLKENIRPFOL 499
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 389 YRITVTAVSASGLASSVYWGPRERELAPLVGPTLWLQDAPPCTPAIANGEVPRHQLRGH 448
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 500 YEIVTPLYQDTPGQSHVAYVSCWAPSHAPEL-HLKHIQGTWAOLEWVPEPELGKSP 558
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 449 LTHYTLCAQSGTSPVCMNVSGMTQSVTLPLDLPWGPCELW-----VTA 491
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 559 LTHYTIFTWNAQNSQSFALINASSRGFVLHGLE--PASLYHIHLMAASQAGATNSIVLTL 616
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 492 STIAGGPGPGPIRLHLPLDNTLRNWKVLPGLFLWGLFLL---GCGLSLATSGRCYHLRKH 548
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 617 MTLTPRGS-----ELHI-----ILGLFGLLLLTCLCG---TAWLCCSPNRK 655
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 549 VLPRAWWEKVPDPANSSG-----OPHMEQVP--EAQPLGDLPITLEVEEMEPVPMES 599
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 656 ----NPLWSPVDPANSSLSGWSWPTIMEEDAFQPLGLGTPPTTKLTVLDEDEKRPV-WES 711
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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QY 600 SOPAQATAPLDSCYKHKFLPTPEELGLL-GPPR 631
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 712 HNSSETCG-----LPTLVQTVVLQGDPR 734
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 15
US-08-419-652-6
; Sequence 6, Application US/08419652
; Patent No. 5831007
; GENERAL INFORMATION:
; APPLICANT: Chua, Anne O
; APPLICANT: Guibler, Ulrich A
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,652
; FILING DATE: 11-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,532
; FILING DATE: 31-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/094,713
; FILING DATE: 19-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: CD 9174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..602
; OTHER INFORMATION: /note= "Represents residues 98 to
; OTHER INFORMATION: 731 of human granulocyte colony-stimulating
; factor-receptor."
; US-08-419-652-6

Query Match      8.4%; Score 294.5; DB 2; Length 602;
Best Local Similarity 22.7%; Pred. No. 4.2e-16;
Matches 149; Conservative 70; Mismatches 240; Indels 197; Gaps 30;

QY 50 LNCSEPLDGLGAPSELHLQSKYRSN-KTQTVAV-----AAGRSWAIPREOLTHMSDKL 103
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 21 LICQWEPGPGTHLPTFTLKSKFSGRCNCQTQGSILDCVPKQGSCHCCIPRKHLLYQNM 80
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 104 LVW-----GKAGQPLW-----PPVEVNLETKMKNAPRLG-----PDVDF 139
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 81 GIWVQAEALGTSMSPOLCLDPMVYKLEPPMLRTWDPSPEAAPQAGCLQLCWEP--- 136
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 140 SEDDPLEATVHMAPTPWPSHKVLICQF-HYRRCQEAANTLLEPELKTPIPTPVEIQDLEL 198
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```



Db 137 -----WOPGLHINQK---CELRRHKPORGEASHALVCP-----LPLEALQYEL 175  
Qy 199 -----ATGYKYVGRCRMEKEEDLWGEWSPILSFQTPPSAPK---DVWYSGNLCGTPPGGEE 250  
Db 176 CGLLPATAYTLQIRIRWPLPGHWSWDSPSLELRTRTERAPTIVRLDTW----- 222  
Qy 251 PLLLWKARGPCVQVSYKYWFVWGGRELSPEGITCCCSLIPSGAEWARVSANVATSWEP-- 308  
Db 223 ----WRQ-----RQDPRTVQLFWKVPVPLEEDSGRIQGY-VVSWRPSG 260  
Qy 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335  
Db 261 QAGAILPLCNTELTSCTHLPSEAOEVALVAYNSAGTSRPTPVVFESEKGPALTRLHAMA 320  
Qy 336 ----ELLVTWQPGGEPLEHVVDWARDGDPLEKLN--WVRLPPGNLSA--LLPGNFTVGYP 388  
Db 321 RDPHSLWGWEPNPWPQGYVIEWGLGPPSASNSKNTWRMEQNGRATGFLLENIRPFQL 380  
Qy 389 YRITVTAVSASGLASASSWGFREELAPLVGPTLWRLQDAPPGTPAIANGEVPRHQLRGH 448  
Db 381 YEIIIVTPLYQDTMGPSQHVYAYSQEMAPSHAPEL-HLKHIGKTAQLEWVPEPPELGKSP 439  
Qy 449 LTHYTLCAQSGTSPSVCMNVSGNTQSVTLPLDPWGPCEIW-----VTA 491  
Db 440 LTHYTFWTNAQNSGFSAILNASSRGFVLHGLE--PASLYHIHLMAASQAGATNSTVLT 497  
Qy 492 STIAQGGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLL---GCGLSLATSGRCYHLRHK 548  
Db 498 MTLTPEGS-----ELHI-----ILGLFGLLLLTCLCG---TAWLCCSPNRK 536  
Qy 549 VLPWRVWEKVPDPANSSG-----QPHMEQVP--EAQPLGDLPILEVEEMEPP 595  
Db 537 ---NPLWPSVPDPAHSSLGSWVPTIMEEDAFQLPGLGTPPTITKLVLEDEKKVP 589

Search completed: May 9, 2002, 06:04:24  
Job time: 36 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search; using sw model

Run on: May 9, 2002, 06:05:05 ; Search time 30.82 Seconds  
(without alignments)  
1539.804 Million cell updates/sec

Title: US-09-692-504-2

Perfect score: 3424

Sequence: 1 MNRRLVARLTPLLELLSLMS.....IVSGYKHFLLPTPEELGLLV 623

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2044	59.7	636	2 JW0047	class I cytokinase
2	277	8.1	1097	2 S17308	leukemia inhibitor
3	270	7.9	918	2 A36337	membrane glycoprot
4	261	7.6	783	2 JH0329	granulocyte colony
5	255.5	7.5	837	2 A34898	granulocyte colony
6	253	7.4	863	2 C38252	granulocyte colony
7	252	7.4	1092	2 JX0312	differentiation-st
8	244	7.1	917	2 I49699	glycoprotein 130
9	228	6.7	771	2 B38252	granulocyte colony
10	223	6.5	918	2 A44257	interleukin-6 sign
11	165.5	4.8	581	2 I45971	prolactin receptor
12	163	4.8	622	2 A40144	Bravo/Nr-CAM cell
13	163	4.8	1259	2 A43425	interleukin-3 rece
14	161	4.7	878	1 A40091	titin, cardiac mus
15	161	4.7	26926	1 I38344	hypothetical prote
16	160.5	4.7	1825	2 T32828	neural cell adhesi
17	158	4.6	1268	1 A39640	leptin receptor, i
18	154	4.5	895	2 S74225	leptin receptor, s
19	153	4.5	892	2 S68439	leptin receptor, s
20	153	4.5	894	2 S88437	leptin receptor, s
21	153	4.5	900	2 S68440	leptin receptor, s
22	153	4.5	1162	2 S68438	leptin receptor, s
23	153	4.5	1197	2 T30581	neural cell adhesi
24	151.5	4.4	2944	2 A54849	collagen alpha 1(V
25	151	4.4	1344	2 T44316	rig-1 protein - mo
26	148	4.3	1162	2 PC4184	leptin receptor, O
27	148	4.3	2477	2 S14428	fibronectin precu
28	146	4.3	13055	2 T16580	hypothetical prote
29	145	4.2	2029	1 TDFFLK	protein-tyrosine-p

ALIGNMENTS

RESULT 1

JW0047

class I cytokinase receptor precursor - human

N:Alternate names: WSX-1

C:Species: Homo sapiens (man)

C:Date: 17-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 21-Jul-2000

C:Accession: JW0047

R:Spiecher, C.A.; Grant, F.J.; Baumgartner, J.W.; Presnell, S.R.; Schrader, S.K.; Yam

Biochem. Biophys. Res. Commun. 246, 82-90, 1998

A:Title: Cloning and characterization of a novel class I cytokine receptor.

A:Reference number: JW0047; MUID:98262921

A:Accession: JW0047

A:Molecule type: mRNA

A:Residues: 1-836 <SPR>

A:Cross-references: GB:AF053004; NID:g3153240; PIDN:AAC39755.1; PID:g3153241

A:Experimental source: brain

C:Genetics:

A:Map position: 19p13.11

C:Keywords: glycoprotein

F:1-32/Domain: signal sequence #status predicted <SIG>

F:515-540/Domain: transmembrane #status predicted <TM>

F:554-561/Domain: cytoplasmic #status predicted <CTP>

F:51.76.302.311.374.382.467/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 59.7%; Score 2044; DB 2; Length 636;

Best Local Similarity 62.8%; Pred. No. 2.2e-133;

Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy 9 LTPLELLLSLLLTGTRPHSGPLQCYSGVGLTNCWEPLGDLTPPVLYHQSKY 68

Db 14 LPKALLPLLVLFQRTQPGSAGPLQCYGVGLDNCWEPLGDLGAPSLHQLQSKY 73

Qy 69 HPNRVWEKVPKQSWVTTPREQFTMAKLLIWTGKGRPLWSSVSNLETQKPDTPQI 128

Db 74 RSNKQTAVAGRSWAIPRLQTLMSDKLLVWGKAGOPLPVPVFNLETQKNAPRL 133

Qy 129 FSQVDISEATLEATVQWAPPVWPQKALTCQFRYKEQAEAWTRLEPOLKTDGLTPVEM 188

Db 134 GPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCEAAWTLLPELKITPTPVEI 193

Qy 189 QNLEPCTCQVSGRCQVENGYP-WGEWSSPLSFQTPFLDPEDVWVSGTVCETSGRAALL 247

Db 194 QDLELATGKVVYGRCKMEEDLWGEWSPILSFQTPPSAPKDVWVSGNLCGTPGGEPL 253

Qy 248 VNKDPRPCQVQTYTVFAGADITTTQEEVPCCKSPVAMWNAWVSPGNSTSWPPTNLS 307

Db 254 LMKAGPCVQVQYKVFVWVGGRRLSPGEGITCCCSLIPSAEAWARVSNATSWEP 313

Qy 308 LVCLAPESAPCDVGVSSADSGPGIKVTKWQGRKPLEYVYVWQDGLSDKLNWTRLP 367

Db 314 LVCLDSASAPRSVAVSSITAGSTELLVTVWPGPEPLEHVVDWARGDPLKLNWRL 373

protein-tyrosine-p

prolactin receptor

prolactin receptor

lactogen receptor

prolactin receptor

plasmacytoma-assoc

fibronectin - Airi

leptin receptor, s

tenascin Y precurs

prolactin receptor

protein-tyrosine-p

Down syndrome cell

prolactin receptor

prolactin receptor

prolactin receptor

MPL-P protein prec





```
FT DOMAIN 519 607 FIBRONECTIN TYPE-III 3.
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 862 AA; 97134 MW; 67C0E0D946B8DD58 CRC64;

Query Match 11.2%; Score 384; DB 1; Length 862;
Best Local Similarity 25.1%; Pred. No. 8,1e-21;
Matches 171; Conservative 88; Mismatches 281; Indels 140; Gaps 33;

QY 5 RVARLTPELLLSMLLGLTRPHGSPGLQCYSGVPLGLTNCWEPGLD--LETPPVLY 62
DB 102 KLACINSDEIQCGAEIFGVAF-E-QPNLSCLQKGEQGVACTWBERGRDTHLYETLQ 160
QY 63 HQSQKYHPRNVVEVK-----VPSKQSWVPIPREQFTWADKLLIWGTQGR 107
DB 161 LSGPK--NLTWQKCKDYCDYLDGFINLTPES-----PESNFAKVTAV-----N 204
QY 108 PLWSSVSVNLETOMKEDTQIFQSDVISEEATLEATVQWAPPVWPP-----QKA----- 156
DB 205 SLGSSSL-----PSTFTFLDI-----VRPLPP-WDIRIKFQKASVRSCTL 244
QY 157 -----LTCQPRYKCOAEATRELPQKTDGLTPVEMONLEPTCY--QVSGRCQVE 206
DB 245 YWRDEGLVLLNRYRPSRSLNMWYN---VTKAGRHLDLDDKPTTEYEFQISSKLHY 301
QY 207 NGYPGWESSPLSFQTFDPE---DWVYSGTVCETSGKRAALLVWK-----DPRPCV-- 256
DB 302 KG-SWDSSESLRAQPEEPTGMDVWYMKRHIDYSRQOISLF-WKNLSVSEARGKILH 359
QY 257 -QVTVYVWFAGDITTTQEEVPCCKSPVAMMEVAV-VSPGNSTSVWPTNLSL--VCLA 312
DB 360 YQVTLQELTGGKAMTQITGHTSWTTVPIRTGNWAVAVSAANSKGSLSLETRINIMLCEA 419
QY 313 PESAPCDVGVSSADGSPGKIVTWKQGRKP---LEVVDWAQ---DGDSDKLNWTRLPP 366
DB 420 GLLAPQVSAANS-EGMDNLVLTWQPRKDPDSAVQEVVWEMRELHPGDDTQVPLNWLRSRP 478
QY 367 GNLSTLLPGCFKGVPIRTVTVAYVSGGLAAPSVMGFREELVPLAGPAVWRPLDDPPGT 426
DB 479 YNVSALISENIKSYICVEIRVYAL-SGDQGGCSSILGNSKHKAPLSGPHINAITEE-KGS 536
QY 427 PVYAVEVPRHQLRGQATHYTFCIQSRGLSTVCVRNYSSTQTATLP-----NLH----- 475
DB 537 ILISWNSIPVQEQMGLLHYRYWKE-----RDSNSQPLCEIPYRVSQNSHPINSLQ 589
QY 476 -SGSFKLWTVTVVAGOGPPDLSLHLPDNRIRKALPWFSLWGLLGMCGLSLASTR 534
DB 590 PRVTVYVLMWLTAAESSHGNREEL-OGKANWMAFVAPSICIAIHWG-----TFSTH 644
QY 535 CLQACLRHWRKHLKQWIERVDPDANSNGQPY-IKEYSLQP-----PRKDGP 593
DB 645 YFOQVFLVLLAALRPQWCSREIPDPANSTCAKKYPYIAEKTQLPLDLLDWDPTPEDPEP 704
QY 584 LEVEEV--ELQPVESPAS 601
DB 705 LVISEVLHQTVPVFRHPPCS 724
```

## RESULT 2

```
IL12S_MOUSE STANDARD; PRT; 874 AA.
ID IL12S_MOUSE
AC P97378;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-
```

```
DE 2) (IL-12R-BETA2).
GN IL12RB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97098510; PubMed=8943050;
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
RA Gately M.K., Gubler U.;
RT "A functional interleukin 12 receptor complex is composed of two
RT beta-type cytokine receptor subunits.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
CC -!- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
CC LOW AFFINITY.
CC -!- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U64199; AAB36676.1; -.
DR HSSP; P40189; 1BQJ.
DR MGD; MGI:1270861; IL12RB2.
DR InterPro; IPR002996; CRJA.
DR InterPro; IPR001777; FN.III.
DR InterPro; IPR003549; Hematopo_rcptor_L_F2.
DR Pfam; PF00411; fn3; 4.
DR PRINTS; PRO0014; FNTYPEIII.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
KW SIGNAL 1 20
FT CHAIN 1 874 INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.
FT DOMAIN 21 639 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 640 656 POTENTIAL.
FT DOMAIN 657 874 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 137 230 FIBRONECTIN TYPE-III 1.
FT DOMAIN 240 322 FIBRONECTIN TYPE-III 2.
FT DOMAIN 436 523 FIBRONECTIN TYPE-III 3.
FT DOMAIN 534 622 FIBRONECTIN TYPE-III 4.
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 874 AA; 98196 MW; 582E4D21BF1FBD67 CRC64;
```

```
Query Match 9.9%; Score 339.5; DB 1; Length 874;
Best Local Similarity 22.1%; Pred. No. 1,6e-17;
Matches 155; Conservative 108; Mismatches 279; Indels 159; Gaps 36;

QY 19 MSLLLTTRPHGSPGLQCYSGVPLGLTNCWEPGLDLETPPVLYHQSKYHPRNVVEVKV 78
```

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:10:49 ; Search time 50.89 Seconds  
(without alignments)  
1790.679 Million cell updates/sec

Title: US-09-692-504-2

Perfect score: 3424

Sequence: 1 MNRRLVARLTPELLLSLMS.....IYSGYKHFLLTPPELGLIV 623

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3424	100.0	623	11 070394	O70394 mus musculus
2	2044	59.7	636	4 O60624	O60624 homo sapien
3	345	10.1	861	6 Q8BEG2	Q8BEG2 bos taurus
4	282	8.2	971	11 O70458	O70458 mus musculus
5	279.5	8.2	970	11 O88821	O88821 mus musculus
6	278	8.1	881	13 O57519	O57519 xenopus lae
7	277	8.1	710	13 O57520	O57520 xenopus lae
8	259	7.6	1093	11 O70535	O70535 rattus norv
9	243.5	7.1	918	13 O9W609	O9W609 gallus gall
10	193.5	5.7	979	4 O96650	O96650 homo sapien
11	167.5	4.9	581	6 O46561	O46561 ovis aries
12	165.5	4.8	296	6 O18880	O18880 bos taurus
13	164	4.8	1140	4 Q9P218	Q9P218 homo sapien
14	163	4.8	1207	4 Q9BQ07	Q9BQ07 homo sapien
15	161.5	4.7	622	6 O9N0J7	O9N0J7 callithrix
16	161	4.7	26926	4 O10466	O10466 homo sapien
17	160.5	4.7	4280	5 Q9UB29	Q9UB29 caenorhabdi
18	160.5	4.7	4450	5 Q9UB28	Q9UB28 caenorhabdi
19	159	4.6	2944	11 O63870	O63870 mus musculus

20	156.5	4.6	1180	4 O15051	O15051 homo sapien
21	155	4.5	2016	5 Q9V4J9	Q9V4J9 drosophila
22	155	4.5	2016	5 Q9NBA1	Q9NBA1 drosophila
23	154.5	4.5	1236	4 Q8UHI3	Q8UHI3 homo sapien
24	154.5	4.5	1308	4 Q8UHI4	Q8UHI4 homo sapien
25	154	4.5	895	11 Q62960	Q62960 rattus norv
26	154	4.5	1162	11 Q9QW63	Q9QW63 mus musculus
27	153.5	4.5	1154	11 Q9QVH3	Q9QVH3 rattus norv
28	153	4.5	1147	13 Q9DDK1	Q9DDK1 meleagris g
29	153	4.5	1197	13 Q90478	Q90478 brachydanio
30	153	4.5	1299	4 O15179	O15179 homo sapien
31	152.5	4.5	1299	4 Q92823	Q92823 homo sapien
32	152	4.4	349	4 Q9UJH5	Q9UJH5 homo sapien
33	151	4.4	1344	11 Q9Z214	Q9Z214 mus musculus
34	149	4.4	625	6 Q9XS92	Q9XS92 trichosurus
35	147.5	4.3	920	4 Q9P232	Q9P232 homo sapien
36	146.5	4.3	1166	11 Q9QVH4	Q9QVH4 rattus norv
37	146.5	4.3	1215	11 P97686	P97686 rattus norv
38	146	4.3	13055	5 Q9N165	Q9N165 caenorhabdi
39	145	4.2	1705	11 Q9ERK5	Q9ERK5 mus musculus
40	145	4.2	2037	5 Q9VIS8	Q9VIS8 drosophila
41	144.5	4.2	2302	11 O88488	O88488 rattus norv
42	142.5	4.2	1028	11 Q07409	Q07409 mus musculus
43	141	4.1	1914	13 Q91008	Q91008 gallus gall
44	139.5	4.1	608	11 Q99J21	Q99J21 mus musculus
45	139.5	4.1	2013	11 Q9ERC8	Q9ERC8 mus musculus

#### ALIGNMENTS

RESULT 1  
O70394  
ID O70394 PRELIMINARY; PRT; 623 AA.  
AC O70394;  
DT 01-AUG-1998 (Tremblrel. 07, Created)  
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)  
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE CLASS I CYTOKINE RECEPTOR.  
GN WSX1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98262921; PubMed=9600072;  
RA Sprecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,  
RA Schrader S.K., Yamagiwa T., Whitmore T.E., O'Hara P.J., Foster D.F.;  
RT "Cloning and characterization of a novel class I cytokine receptor.";  
RL Biochem. Biophys. Res. Commun. 246:82-90(1998).  
DR EMBL; AF053005; AAC40121.1;  
DR MGD; MGI:1355318; Wsx1.  
DR InterPro; IPR003961; FN\_III.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
SQ SEQUENCE 623 AA; 68998 MW; 4BA20FEC875A7180 CRC64;

Query Match 100.0%; Score 3424; DB 11; Length 623;  
Best Local Similarity 100.0%; Pred. No. 1.3e-261;  
Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNRRLVARLTPELLLSLMSLLLTGRPHGSPGLOCYSVGPLGILNCSEPLGDLTPPV	60
Db	1	MNRRLVARLTPELLLSLMSLLLTGRPHGSPGLOCYSVGPLGILNCSEPLGDLTPPV	60
Qy	61	LYHQSKYHPNRVWEKVPKSWVTIPREQFTMDKLLIWGTQGRPLWSSVSVNLEQ	120
Db	61	LYHQSKYHPNRVWEKVPKSWVTIPREQFTMDKLLIWGTQGRPLWSSVSVNLEQ	120
Qy	121	MKPDPTQIFSQVDISEATLEATVQWAPPVPPQKALTCQFRYKECOAEAWTRLEPQ	180

Db	121	MKPDTPQIFSQVDISEATLEATVQWAPPVWPQKALTCQFRYKECAEAWTRLEPQLKT	180
QY	181	DGLTPVEMQNLEPGTCYQVSGRCQVNGYPWGEWSSPLSFQTPFLDPEDVWVSGTCVETS	240
Db	181	DGLTPVEMQNLEPGTCYQVSGRCQVNGYPWGEWSSPLSFQTPFLDPEDVWVSGTCVETS	240
QY	241	GKRAALLVWKDPRPCVQVYTYVWFGAGDITTTQEEVPCCKSPVPAMWNAVSPGNSTSW	300
Db	241	GKRAALLVWKDPRPCVQVYTYVWFGAGDITTTQEEVPCCKSPVPAMWNAVSPGNSTSW	300
QY	301	VPTNLSLVCLAPESAPCDGVSSADGSPGKIVTWKQGRKPLLEYVVDNAQDGSLSLKLIN	360
Db	301	VPTNLSLVCLAPESAPCDGVSSADGSPGKIVTWKQGRKPLLEYVVDNAQDGSLSLKLIN	360
QY	361	WTRLPNGLSTLLPGFKGVPVRIITVAVYSGGLAAAPSVMGFREELVPLAGPAWRPLP	420
Db	361	WTRLPNGLSTLLPGFKGVPVRIITVAVYSGGLAAAPSVMGFREELVPLAGPAWRPLP	420
QY	421	DPPGTPVAVWGEVPRHQLRGQATHYTCIQSRGLSTVCNRNVSSTQTATLPLNLHSGSEK	480
Db	421	DPPGTPVAVWGEVPRHQLRGQATHYTCIQSRGLSTVCNRNVSSTQTATLPLNLHSGSEK	480
QY	481	LWTVSTVAGOGPPGDLSLHLDPNRIRKALPWFUSLWGLLMLGCGLSLASTRCLQARC	540
Db	481	LWTVSTVAGOGPPGDLSLHLDPNRIRKALPWFUSLWGLLMLGCGLSLASTRCLQARC	540
QY	541	LHWRHRLLPQWIWERYVDPANSHSGOPYIKEYSLPQPKDGPILVEEVEELQPVVESPRA	600
Db	541	LHWRHRLLPQWIWERYVDPANSHSGOPYIKEYSLPQPKDGPILVEEVEELQPVVESPRA	600
QY	601	SAPIYSGYKHFLLPTPEELGLLV 623	
Db	601	SAPIYSGYKHFLLPTPEELGLLV 623	
RESULT	2		
QY	060624	PRELIMINARY; PRT; 636 AA.	
AC	060624;		
DT	01-AUG-1998 (TREMBLrel. 07, Created)		
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	CLASS I CYTOKINE RECEPTOR (CRLI PROTEIN).		
GN	WSX1 OR CRLI.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OY	NCBI_TaxID=9606;		
RA	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE:98262921; PubMed=9600072;		
RA	Sprecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,		
RA	Schraeder S.K., Yamagiwa T., Whitmore T.E., O'Hara P.J., Foster D.F.;		
RT	"Cloning and characterization of a novel class I cytokine receptor.";		
RL	Biochem. Biophys. Res. Commun. 246:82-90(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Zhang W., Wan T., He L., Yuan Z., Cao X.;		
RT	"A novel gp130-like cytokine receptor.";		
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF053004; AAC39755.1; -.		
DR	EMBL; AF106912; AAG26090.1; -.		
DR	InterPro; IPR003961; FN_III.		
DR	Pfam; PF00041; fn3; 2.		
DR	SMART; SM00060; FN3; 1.		
SQ	SEQUENCE 636 AA; 69473 MW; DC7DAAAABA643CE97 CRC64;		
Query Match	59.7%;	Score 2044;	DB 4; Length 636;
Best Local Similarity	62.8%;	Pred. No. 7e-153;	
Matches	398;	Conservative 61;	Mismatches 161; Indels 8; Gaps 3;

9 LTPLELLLSLMSLLLTRPHSGSPGLQCYSGVGLGLNCSWEPLGLDTPPVLYHOSQXY 68

Db	14	LPKALLPLLWLFQTRPGSAGPLQCYGVPGLDNCWEPGLDGLAPSELHLSQXY	73
QY	69	HNRYWEVVPKQSWVTIPREQFTMADKLLTWGQKGRPLASSVSVNLETOMKPDTPQI	128
Db	74	RNKQTQTVAAAGRSWALPREQLTMSDKLLVWGTAGQPLWPPVFNLETOMKNAPRL	133
QY	129	FSQVDISEATLEATVQWAPPVWPQKALTCQFRYKECAEAWTRLEPQLKDTGLTPVEM	188
Db	134	GPVDVDFSEDDPLEATVHMAPTWPSHKVLICQHYRRCCOEAATWLTLEBELKTIPLTPEI	193
QY	189	QNLPGTCTCVSGRCOVENGYP-WGEWSSPLSFQTPFLDPEDVWVSGTCVETSGKRAALL	247
Db	194	QDLLEATGKYKTVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSGNLCGTPGGEPLL	253
QY	248	VNKDRPCVQVYTYVWFGAGDITTTQEEVPCCKSPVPAMWNAVSPGNSTSWPPTNLS	307
Db	254	LWKAQPCQVQSVKVMFWVGGRELSPEGITCCCSLIPSGAEWARVSAVWATSWEPITNLS	313
QY	308	LVCLAPESAPCDGVSSADGSPGKIVTWKQGRKPLLEYVVDNAQDGSLSLKLINWTRLP	367
Db	314	LVCLDSASAPRSVAVSSVAGSTELLVWQPGCEPLEHVVDWARDGPLEKLNWVRLPPG	373
QY	368	NLSTLLPGGEFGVYRITVAVYSGGLAAAPSVMGFREELVPLAGPAWRPLPDDPGTP	427
Db	374	NLSALLPGNFTVQVYRITVAVSASGLASASSVMGFREELAPLVGPTLWRLQDAPP	433
QY	428	VWANGVPRHQLRGQATHYTCIQSRGLSTVCNRNVSSTQTATLPLNLHSGSFKLWTVST	487
Db	434	ATANGVPRHQLRGQATHYTCIQSRGLSTVCNRNVSSTQTATLPLNLHSGSFKLWTVST	493
QY	488	VAGQPPGDLSLHLDPNRIRKALPWFUSLWGLLMLGCGLSLASTRCLQARCLHWRHKL	547
Db	494	IAGQPPGDLRLHLPDNTLRNKLPGILFGLGLFLGLGGLSLATS-GRYHLRHKV	549
QY	548	LPQWIWERYVDPANSHSGOPYIKEYSLPQPKDGPILVEEVEELQPVVETS-PRASAPI	604
Db	550	LPRWWEKYVDPANSSGQPHMEQVPEAQPLGLDLPILVEEVEEPPVMESSQPAQATPL	609
QY	605	YSGYKHFLLPTPEELGLL 622	
Db	610	DSGYKHFLLPTPEELGLL 627	
RESULT	3		
QY	09BEG2	PRELIMINARY; PRT; 861 AA.	
AC	09BEG2;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DE	IL-12 RECEPTOR BETA2 PRECURSOR.		
GN	IL-12R BETA2.		
OS	Bos taurus (Bovinae).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
OY	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LYMPH NODE;		
RA	Waldbogel A.S., Zakher A., Heussler V.T.;		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ308426; CAC28320.1; -.		
KW	Signal; Receptor.		
FT	SIGNAL 1 23 POTENTIAL.		
SQ	CHAIN 24 861 IL-12 RECEPTOR BETA2.		
SQ	SEQUENCE 861 AA; 96208 MW; 4B7B1E5D1E358E5B CRC64;		
Query Match	10.1%;	Score 345;	DB 6; Length 861;
Best Local Similarity	23.7%;	Pred. No. 7.4e-19;	
Matches	159;	Conservative 110;	Mismatches 297; Indels 106; Gaps 35;



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:06:12 ; Search time 43.01 Seconds  
(without alignments)  
1072.952 Million cell updates/sec

Title: US-09-692-504-2

Perfect score: 3424

Sequence: 1 MNRLRVARLTPELLLSLMS.....IYGVKFKFLPTPEELGLLV 623

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_ll01.\*

1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3424	100.0	623	19 AAW33400	Mouse haematopoiet
2	3424	100.0	623	22 AAU01854	Mouse type I cytok
3	2044	59.7	636	19 AAW33399	Alternatively spli
4	2044	59.7	636	22 AAU01853	Human type I cyto
5	2036	59.5	636	20 AAY29781	Human DNAX cytokin
6	1866.5	54.5	578	19 AAW33398	Human haematopoiet
7	1720	50.2	523	20 AAY29785	Partial human DNAX
8	1342	39.2	246	20 AAY29786	Partial mouse DNAX
9	712	20.8	150	20 AAY29782	Mouse DNAX cytokin
10	384	11.2	862	18 AAW12771	Human interleukin-
11	280	8.2	1001	13 AAR25068	hLIF-R, Homo sapi

12	277	8.1	1097	15	AAAR49508	Human LIF-R. Homo
13	277	8.1	1097	15	AAAR45776	Human leukaemia in
14	277	8.1	1097	16	AAAR74097	Human leukaemia in
15	276	8.1	1001	15	AAAR45774	Human leukaemia in
16	275	8.0	1001	14	AAAR37806	Human LIF-R N-term
17	272	7.9	1001	16	AAAR4095	Human leukaemia in
18	270	7.9	708	17	AAAR5911	gp130 N-terminal f
19	270	7.9	918	12	AAAR10545	Recombinant human
20	270	7.9	918	15	AAAR46233	Granulocyte colony
21	270	7.9	918	21	AAAY44694	Human placental G-
22	269	7.9	1001	15	AAAR49506	Human granulocyte
23	264	7.7	918	17	AAAR5368	Human LIF-R clone
24	261	7.6	708	14	AAAR37804	Human gp130 protei
25	261	7.6	783	12	AAAR11741	Human gp130 N-term
26	261	7.6	783	16	AAAR77868	Granulocyte colony
27	261	7.6	783	18	AAAW10485	Human placental G-
28	261	7.6	800	18	AAAW10486	Human granulocyte
29	261	7.6	801	12	AAAR11742	Clone 25-1 encoded
30	261	7.6	813	21	AAAB03873	Human granulocyte
31	260	7.6	836	12	AAAR14255	Human GCSF recepto
32	259.5	7.6	837	12	AAAR14254	Murine GCSF recept
33	253.5	7.4	1522	16	AAAR70125	LIF-R-GSP 130 fusi
34	252	7.4	863	12	AAAR14257	Human GCSF recepto
35	247	7.2	662	22	AAAB51244	Human haemopoietin
36	246.5	7.2	873	22	AAAU02905	Angiotensin conver
37	244	7.1	652	22	AAAB51242	Human haemopoietin
38	244	7.1	917	13	AAAR36334	Human haemopoietin
39	244	7.1	917	21	AAAY55073	gp130. Mus muscul
40	232.5	6.8	775	22	AAAU02904	Mouse gp130 protei
41	228	6.7	824	22	AAAM3678	Angiotensin conver
42	227	6.6	771	12	AAAR14256	Human EST encoded
43	226	6.6	658	17	AAAR94576	Human GCSF recepto
44	224.5	6.6	727	21	AAAY92192	Human gp130-splice
45	224.5	6.6	738	21	AAAY92194	Human gp130-kappa

#### ALIGNMENTS

RESULT 1  
AAW33400  
ID AAW33400 standard; Protein: 623 AA.  
AC AAW33400;  
DT 22-MAY-1998 (first entry)  
DE Mouse haematopoietic cytokine receptor Zcytor1.  
DE Mouse haematopoietic cytokine receptor Zcytor1; ligand detection;  
KW Mouse; haematopoietic cytokine receptor; Zcytor1; agonist; antagonist; murine.  
OS Mus sp.  
PN WO9744455-A1.  
XX  
XX 27-NOV-1997.  
XX  
XX 19-MAY-1997; 97WO-US08502.  
XX  
XX 23-MAY-1996; 96US-0653740.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;  
XX  
XX WPI; 1998-018509/02.  
XX  
XX N-PSDB; AAT94121.  
XX  
XX Haematopoietic cytokine receptor - useful for ligand detection, and  
XX pathological condition diagnosis  
XX  
XX Claim 3; Pages 54-58; 86pp; English.

```

XX CC The present sequence is the mouse haematopoietic cytokine
CC receptor Zcytor1, useful for ligand detection, and pathological
CC condition diagnosis, including cancer. Receptor agonists of the
CC protein can be used to stimulate the proliferation and development
CC of target cells in vitro and in vivo. The agonists can stimulate
CC cell mediated immunity and lymphocyte proliferation, to treat
CC infection involving immunosuppression, e.g. viral infections. They
CC may also be used to suppress tumours, induce cytotoxicity, treat
CC leukopenias and enhance the regeneration of the T-cell repertoire
CC after bone marrow transplantation. Antagonists of the protein may
CC be used to suppress the immune system, treat autoimmune diseases,
CC including rheumatoid arthritis, multiple sclerosis and diabetes
CC mellitus. Immune suppression caused by the antagonists can also be
CC used to reduce rejection of tissue or organ transplants and grafts,
CC and to treat T-cell specific leukaemias and lymphomas.
XX SQ Sequence 623 AA:
      1  MNRLVARLTPLLELLSLMSLLIGTRPHSGPGLQCYSGPLGILNCSEPLGDLTPPV 60
      1  mnrlrvarltpllellslmslllgttrphsgpgplqcysvpgilncswepldgletppv 60
QY 61  LYHQSKYHNPVRWEVKVSKSWIIPREQFTMDKLLIWTQKRPPLWSSVSNLEQTQ 120
DB 61  lyhqskqyhnprwewkvpskswitipreqftmdklllwtqtkrplwssvsnletq 120
QY 121 MKPDTQIFQSDVISEATLEAIVQWAPPVWPPOKALTQCFYKCEQAAWTRLEPOLKT 180
DB 121 mkpdtqifsqvdiseatleavqwapvpwpqokaltcfykykceqaawtrlepolkt 180
QY 181 DGLTPVEMQNLEPGTCYQVSGRCQVNGYPMGEWSSPLSFQTPFLDPEDVWVGTYCETS 240
DB 181 dgltpvemqnlepgtcyqvsgrcqvngypmgewssplsfqtpfldpedvwwsgtycets 240
QY 241 GKRAALLVWKDPRCPQVQVYTVWFAGDITTTQEEVPCCKSPVPAWMEWAVSPGNSTSW 300
DB 241 gkraallvwkdprrcpvqvvtvfwfagdtittqeevpcckspvpawmewavspgnstsw 300
QY 301 VPPTNLISLVLAPESAPCDVGVSSADGSPGKVTWKQGRKPLEYVVDWAQDGDSDLKLN 360
DB 301 vpptnlislvlapesapcdvgvssadgsgpgkvtwkqgrkpleyvvdwaqgdgdsldkln 360
QY 361 WTRLPFGNLSTLLPGEFGKGVPIRVITVAVYSGGLAAAPSVWGFREELVPLAGPAWRRLP 420
DB 361 wtrlpfgnlstllpgfkggvpiyritvavysgglaaapsvwgfreetvplagpavwrilp 420
QY 421 DDPGCTPVVAVGEPVRHQLRGQATHYTFCTIOSKGLSTVCNRVSSQFTATLNLHSGSEPK 480
DB 421 ddpdgctpvvavgepvvrhqlrgqathytfctioskglstvcnrnvssqftatlnlhsgsepk 480
QY 481 LWTVSTVAGQGGPDLHLPLDNRIRKALPWFLSLWGLLMLGCLSLASTRCLQARC 540
DB 481 lwvtstvagqggpdlhlpldnrirkalpwlflslwglmlgclslastrclqarc 540
QY 541 LHWRRKLLPQWIWERYPDPANNSGOPYIKEVSLPOPCKDGPILVEVEVELQPVWESPKA 600
DB 541 lwhrrkllpqwiwerypdpansngopyikevslpopckdgpilveevevelqpvwespska 600
QY 601 SAPIYSGYEKHFLPTPEELGLLV 623
DB 601 sapiysgyekhfllptpeeigllv 623
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RESULT 2  
AAU01854  
ID AAU01854 standard; Protein; 623 AA.  
XX

```

AC AAU01854;
XX 07-SEP-2001 (first entry)
XX Mouse type I cytokine receptor, mTCCR.
XX Mouse; type-I cytokine receptor; TCCR; T-cell differentiation;
KW Th1; Th2; agonist; antagonist; autoimmune inflammatory disease;
KW allograft rejection; multiple sclerosis; inflammatory bowel disease;
KW insulin-dependent diabetes mellitus; infectious disease;
KW human immunodeficiency virus; allergic disorder; asthma;
XX allergic rhinitis; HIV.
OS Mus musculus.
FH Key
FT Peptide
FT /label= Signal_peptide
FT /note= "Casein kinase II phosphorylation site"
FT Region
FT /note= "Region of homology to human erythropoietin"
FT Protein
FT /label= Mature_mTCCR
FT Region
FT /note= "Cytokine receptor family signature 1"
FT Modified-site
FT /label= N_myristoylation_site
FT Modified-site
FT /note= "Asn is N-glycosylated"
FT Modified-site
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site
FT /label= N_myristoylation_site
FT Modified-site
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site
FT /note= "Tyrosine kinase phosphorylation site"
FT Region
FT /note= "Region of homology with murine interleukin-5 receptor"
FT Modified-site
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site
FT /label= Amidation_site
FT Modified-site
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site
FT /note= "Asn is N-glycosylated"
FT Modified-site
FT /note= "Asn is N-glycosylated"
FT Modified-site
FT /label= N_myristoylation_site
FT Modified-site
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site
FT /label= N_myristoylation_site
FT Modified-site
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FT /note= "Asn is N-glycosylated"
FT Modified-site
FT /label= N_myristoylation_site
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FT Modified-site 461..464  
 FT Domain /note= "Asn is N-glycosylated"  
 FT 514..532  
 FT /label= Transmembrane\_domain  
 FT Modified-site 516..526  
 FT /note= "Prokaryotic membrane lipid attachment site"  
 FT Modified-site 525..530  
 FT /label= N\_myrystoylation\_site  
 FT Modified-site 527..532  
 FT /label= N\_myrystoylation\_site  
 FT Modified-site 606..609  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 615..618  
 FT /note= "Casein kinase II phosphorylation site"  
 XX  
 PN WO200129070-A2.  
 XX  
 XX 26-APR-2001.  
 PD  
 XX 18-OCT-2000; 2000WO-US28827.  
 XX  
 XX 20-OCT-1999; 99US-0160542.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX De Sauvage FJ, Grewal I, Gurney AL;  
 PI  
 XX WPI; 2001-308474/32.  
 DR N-PSDB; AAS03263.  
 DR  
 XX  
 XX Modulating T-cell differentiation and cytokine release profiles into  
 FT Th1 and Th2 subtypes, for treating immune-related diseases in mammals,  
 FT by administering modulator of type I cytokine receptor (TCR) -  
 XX  
 XX Example 1; Fig 4; 126pp; English.  
 XX  
 CC The sequence represents mouse type I cytokine receptor, mTCR. The  
 CC invention relates to methods of modulating the differentiation of  
 CC T-cells into the Th2 subtype instead of the Th1 subtype, by  
 CC administering a modulator of TCR (e.g. an antagonist) to enhance,  
 CC stimulate or potentiate T-cell differentiation, or using TCR  
 CC polypeptide or its agonists to prevent, inhibit or attenuate T-cell  
 CC differentiation. Th1 mediated disease in mammal can be treated by  
 CC administering a TCR antagonist and Th2 diseases by administering a TCR  
 CC agonist. Th1-mediated diseases include allograft rejection and autoimmune  
 CC inflammatory diseases, such as allergic encephalomyelitis, multiple  
 CC sclerosis, insulin-dependent diabetes mellitus, autoimmune uveoretinitis,  
 CC inflammatory bowel disease or autoimmune thyroid disease. Th2-mediated  
 CC diseases include infectious diseases, such as Leishmania major,  
 CC Mycobacterium leprae, Candida albicans, Toxoplasma gondii, respiratory  
 CC syncytial virus and human immunodeficiency virus (HIV) and allergic  
 CC disorders, such as asthma, allergic rhinitis, dermatitis and vernal  
 CC conjunctivitis.  
 XX  
 SQ Sequence 623 AA;  
  
 Query Match 100.0%; Score 3424; DB 22; Length 623;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-265;  
 Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 MNRRLVRLTLELLLSLMSLLGTRPHGSPGLQCYSGVPLGLNCSWEPLGDLTEPPV 60  
 Db 1 mnrilrvartlpllellslmslllgrphgspglqcyvgplglncswepglgdlteppv 60  
 Qy 61 LYHGSQKYHPRNVRWEKVPKQSWVTIPREQFTMDKLLIWTQKGRPLWSVSVNLETQ 120  
 Db 61 lyhgsqkyhprnvrwekvpkqswvtipreqftmdklliwgtqkgrplwsvsvnletq 120  
 Qy 121 MKPDPQIFSQVDISEEATLEATVQWAPPVPPQKALTCQRYKCEQAEATWRLPEQLKT 180  
 Db 121 mkpdpqifsqvdisseetleatvqwapppvppqkaltcqrykcegaeatwrlpeqlkt 180

Qy 181 DGLTPVENQNLPEPGTCYQVSGRCQVENGYPMGEWSPLSFQTFPLDPEDVWVSGTVCETS 240  
 Db 181 dgltpvenqnlpepgtcyqvgvgrcqvengypmgewspisfqtcpfldpedvwwsgtvcets 240  
 Qy 241 GKRAALLVWKDPRPCVQVYTYVWFCAGDITTTQEEVPCKCKSPVPAMMEWAVVSPGNSISW 300  
 Db 241 gkraallvwkdprpcvcvqvtvtwfgagdtittqeevpckckspvpamwewavvspgnsisw 300  
 Qy 301 VPPTNLSLVCLAPESAPCDVGSADGSPGKIKVTWKQGRTRKPLEYVVDWAQDGLDLKLN 360  
 Db 301 vpptnlsivclapesapcdvgvsadgspgikvtwkqgrtrkpleyvvvwaqdgldldkln 360  
 Qy 361 WTRLPDGNLSTLLPGEFKGGVPYRITVAVYSGGLAAAPSVWGFREELVPLAGPAVWRUP 420  
 Db 361 wtrlpdgnlstllpgfefkggvpvritvavysgglaaapsvwgfreelvplagpavwrup 420  
 Qy 421 DDPGTTPVWANGVEPRHOLRGOATHYTCIQSRGLSTVCRNVSSQTATLPLNLSGSEFK 480  
 Db 421 ddpgtpvawangevprhqlrgqathyticdrgslstvcvrvssqtatlpnlhsgsfk 480  
 Qy 481 LWVTYSTVAGOGPPGDLSLHLPDNRIRWKPFLSLWGLLMLGGLSLASTRCLQARC 540  
 Db 481 lwtvtstvagoggpdlslhlpdnrirkwkalpwlslwglmlgglslastrclqarc 540  
 Qy 541 LHWHRKLLPQWIWERVDPDANSNGQPYIKEYSLPQPKDGPILVEVEVELOPVVESPKA 600  
 Db 541 lwhrhkllpqwiwervdpdansngqpyikevslppkdgpileveeveelqpvvespka 600  
 Qy 601 SAPIYSGYEKHFLLPTPEELGLLV 623  
 Db 601 sapiysgyekhfllptpeelglilv 623  
 RESULT 3  
 AAW33399  
 ID AAW33399 standard; Protein; 636 AA.  
 AC AAW33399;  
 DT 22-MAY-1998 (first entry)  
 DE Alternatively spliced zcytor1.  
 KW Human; haematopoietic cytokine receptor; zcytor1; ligand detection;  
 KW cancer diagnosis; agonist; antagonist; alternatively spliced.  
 OS Homo sapiens.  
 PN WO9744455-A1.  
 PD 27-NOV-1997.  
 PF 19-MAY-1997; 97WO-US08502.  
 PR 23-MAY-1996; 96US-0653740.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;  
 XX WPI; 1998-018509/02.  
 DR N-PSDB; AAT94120.  
 FT Haematopoietic cytokine receptor - useful for ligand detection, and  
 FT pathological condition diagnosis  
 PS Claim 7; Pages 46-51; 86pp; English.  
 CC The present sequence is an alternatively spliced human  
 CC haematopoietic cytokine receptor zcytor1, useful for ligand  
 CC detection, and pathological condition diagnosis, including cancer.  
 CC Receptor agonists of the protein can be used to stimulate the  
 CC proliferation and development of target cells in vitro and in vivo.

CC The agonists can stimulate cell mediated immunity and lymphocyte  
CC proliferation, to treat infection involving immunosuppression, e.g.  
CC viral infections. They may also be used to suppress tumours, induce  
CC cytotoxicity, treat leukopenias and enhance the regeneration of  
CC the T-cell repertoire after bone marrow transplantation.  
CC Antagonists of the protein may be used to suppress the immune  
CC system, treat autoimmune diseases, including rheumatoid arthritis,  
CC multiple sclerosis and diabetes mellitus. Immune suppression caused  
CC by the antagonists can also be used to reduce rejection of tissue  
CC or organ transplants and grafts, and to treat T-cell specific  
CC leukaemias and lymphomas.

XX  
SQ Sequence 636 AA;

Query Match 59.7%; Score 2044; DB 19; Length 636;  
Best Local Similarity 62.8%; Pred. No. 6.7e-155;  
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

QY 9 LTPLELLLSLLGTRPHSGPLQCYSGPLGLINGSWEPLGDLTPPPVLYHQSQRY 68  
DB 14 lpklaillpllwlfqtrpgsgugplqcygvpplgdlncswepplgdlgapsehlqsqky 73  
QY 69 HPNRWVEVYKQSQWYTPREQFTWADKLLIWGTOKGRPLWSSVSNLETKMKPTPOI 128  
DB 74 rsnktqtvaagrswwaipreqltmsdkllwgtkagqplwppvfnletgmknprzl 133  
QY 129 FSOVDISEATLEATVQWAPVPPVPPKATCFPRYKCCQAEATWRLPKLTDGLTPVEM 188  
DB 134 gpdvdseddpateatwhapptwpskvlfcqfhyrcqeaawlllepelktpitpvel 193  
QY 189 QNLEPTCYQVSGRCOVENGY-P-WGSWSPLSFQTPFLDPEDVWVSCTVCSGKRAALL 247  
DB 194 qdletatgykvygrcmekeedlwgespllsftqpsapkdvwsngnlgctpggeepil 253  
QY 248 VKMDRRCQVYTVWFGAGDITTTQEEVPCCKSPVPAWMEWAVSPGNSWVPPTNLS 307  
DB 254 lwkagpvcvqsykvwfwggrralspegitcccllpsgaewarvsavnatsewepitnls 313  
QY 308 LVCLAPESAPCDVGSASDGSPIKVTWKGTRKPLEYVVDNAQDGLDKLWTRLP 367  
DB 314 lvcldasaprsvvasisagstetllvtwpgpgpgeplehvwrdardgplekinwvrlppg 373  
QY 368 NLSTLLPFGFKGVPYRIYTVAVISGLAAPSVMGFEELVPLAGPAYVWRLPDDPPGTP 427  
DB 374 nlsallpgnftvgpyritvatsasglaasvswfreeslplvgptlwrldapgtcp 433  
QY 428 VWANGVPRHLRGQATHYTFQTSRGLSTVCRNVSSQTATPLNLSGSKLWTVTST 487  
DB 434 alawgevprhlrghlthylclsqsgtspscvmvsgntqsvtlpdlwpgpcelwvtast 493  
QY 488 VAGQGPDPGLSLHLPDNRIRKALPWFSLMGLLLMGLSLASTPCLOARCLHWRHL 547  
DB 494 iagggppgplrlhupdntrkwlpgllflwgflfllcgslats---grcyhlrhkv 549  
QY 548 LPQWIERVPDPANSNSGOPYIKEVSLPPKDPKDPILVEVEELQPVVES---PKASAPI 604  
DB 550 lprwvewkvpdpansngpshmeqveacplgdlplileveempppvmesspaqatapl 609  
QY 605 YSGYKHFLPTPEELGLL 622  
DB 610 dsgyekhflptpeelgll 627

RESULT 4

AAU01853  
ID AAU01853 standard; Protein; 636 AA.  
XX  
AC AAU01853;  
XX  
DT C7-SEP-2001 (first entry)  
XX Human type I cytokine receptor, hTCCR.

XX Human; type-I cytokine receptor; TCCR; T-cell differentiation;  
KW Th1; Th2; agonist; antagonist; autoimmune inflammatory disease;  
KW allograft rejection; multiple sclerosis; inflammatory bowel disease;  
KW insulin-dependent diabetes mellitus; infectious disease;  
KW human immunodeficiency virus; allergic disorder; asthma;  
KW allergic rhinitis; HIV.  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..32  
FT Protein 33..636  
FT Mature\_hTCCR  
FT Region 41..54  
FT Note= "Cytokine receptor family signature 1"  
FT Modified-site 51..54  
FT Note= "Asn is N-glycosylated"  
FT Modified-site 76..79  
FT Note= "Asn is N-glycosylated"  
FT Modified-site 107..112  
FT Note= "N-myristoylation\_site"  
FT Region 183..191  
FT Note= "Region of homology with the second subunit  
of human granulocyte-macrophage colony-stimulating  
factor"  
FT Modified-site 240..245  
FT Note= "N-myristoylation\_site"  
FT Modified-site 244..249  
FT Note= "N-myristoylation\_site"  
FT Modified-site 281..286  
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FT Modified-site 467..470  
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FT Domain 517..538  
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FT Modified-site 533..538  
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FT Modified-site 563..566  
FT Note= "Asn is N-glycosylated"  
XX  
PN WO200129070-A2.  
XX  
XX PD 26-APR-2001.  
XX  
XX PF 18-OCT-2000; 2000WO-US28827.  
XX PR 20-OCT-1999; 99US-0160542.  
XX PA (GETH ) GENE TECH INC.



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Query Match      59.5%; Score 2036; DB 20; Length 636;
Best Local Similarity 62.5%; Pred.No. 2.9e-154;
Matches 386; Conservative 62; Mismatches 162; Indels 8; Gaps 3;

QY 9 LTPLELLLSMLLLGTRPHGSPGLQCYSGVPLGLNCSWEPLGDLTPPPVLYHQSQKY 68
DB 14 lpklaillplwlfgrtrpqgsagplqcyvgplgdlncsweplgdlgapshelhqsky 73
QY 69 HPNRWEVKVPKSKQSWITPRQFTMADKLLIWGTQKGRPLWSSVSNLETKMPTPOI 128
DB 74 rsnktqtvaagrsawaipreqlmsdkllwvqkagqplwppvfvnletgmknapi 133
QY 129 FSQVDISEATLEATVQWAPPVWPQKALTCQFRYKECAEAWTRLEPOLKTDGTPVEM 188
DB 134 gpdvfdsedpdeatvhwappwpskhvliqcfryrqcaawtllpeelktiptpei 193
QY 189 QNLEPGTCYQVSGRCQVGENYP-WGEWSSPLSFQTFPFLDPEDVWVSGTVCETSGRAALL 247
DB 194 qdeleatgykyvgrcrmekeedlwgepslilsfqtppsapkdvwvsgnlcgtppgeep 253
QY 248 VMDPRPCVQVITYVWFGAGDITTTQEEVPCKSPVPAWMEWAVSPGNSTSWVPPTNLS 307
DB 254 lwkagpcvqvykvwfwvgrrelspegitccclipsgaeavrsavnatsewptnls 313
QY 308 LVCLAPESAPCDVGVSSADGSPGIKVTWKQGRKPLEYVVDWAQDGLSKLWTRLPVEM 367
DB 314 lvcldsaaprsvavssilagsteillvtwqpggeplehvmwdardgplekinwrlppg 373
QY 368 NLSTLLPGFEKGGVPYRTVTAVYSGGLAAAPSVWGFREELVPLAGPAVWRLPDDPPGTP 427
DB 374 nlsallpgnftvgvpyriltvavssaglasavsvwgfrelaplvgtlwrldqappgcp 433
QY 428 VYAWGEVPRHQRLQGATHYTFICIQSRGLSTVCRNVSSQTQTATLPNLHSGSFKLWTVST 487
DB 434 alawgevrhqlrghlthyltcaqgstpsvcmvsgntqstvtlpldwpgpcelwvtast 493
QY 488 VAGQPGPGDLSHLPLDNRIRKALPWFILSLWGLLWGLLWGLSLASTRCLQARCLHWRHKL 547
DB 494 laggpgppilrhipdntlrwkvlpglflwglfllgclslats----grcyhlrhkv 549
QY 548 LPQWIERVPDPANSSNGOPYIKVSLPQPKDGPILVEEVELOPVVES---PKASAPI 604
DB 550 lprwwekvpdpansssgqphmeqvpeaqplgdplileveempppvmeassqagatapi 609
QY 605 YSGYEKHFLLPTPEELGLL 622
DB 610 dsygekhlftpeelgl 627

RE 6
AAW33398
XX AAW33398 standard; Protein; 578 AA.
XX AC AAW33398;
XX AC AAW33398;
XX DT 22-MAY-1998 (first entry)
XX DE Human haematopoietic cytokine receptor zcytor1.
XX KW Human; haematopoietic cytokine receptor; zcytor1; ligand detection;
XX KW cancer diagnosis; agonist; antagonist.
XX OS Homo sapiens.
XX PN WO9744455-A1.
XX XX 27-NOV-1997.
XX XX 19-MAY-1997; 97MO-US08502.
XX PR 23-MAY-1996; 96US-0653740.
XX XX (ZYMO ) ZYMOGENETICS INC.
```

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XX Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;
XX WPI: 1998-018509/02.
XX N-PSDB; AAT94119.
XX Haematopoietic cytokine receptor - useful for ligand detection, and
XX pathological condition diagnosis
XX Claim 1; Pages 39-43; 86pp; English.
XX The present sequence is the human haematopoietic cytokine
XX receptor zcytor1, useful for ligand detection, and pathological
XX condition diagnosis, including cancer. Receptor agonists of the
XX protein can be used to stimulate the proliferation and development
XX of target cells in vitro and in vivo. The agonists can stimulate
XX cell mediated immunity and lymphocyte proliferation, to treat
XX infection involving immunosuppression, e.g. viral infections. They
XX may also be used to suppress tumours, induce cytotoxicity, treat
XX leukopaenias and enhance the regeneration of the T-cell repertoire
XX after bone marrow transplantation. Antagonists of the protein may
XX be used to suppress the immune system, treat autoimmune diseases,
XX including rheumatoid arthritis, multiple sclerosis and diabetes,
XX mellitus. Immune suppression caused by the antagonists can also be
XX used to reduce rejection of tissue or organ transplants and grafts,
XX and to treat T-cell specific leukaemias and lymphomas.
XX Sequence 578 AA;
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Query Match      54.5%; Score 1866.5; DB 19; Length 578;
Best Local Similarity 61.7%; Pred.No. 9e-141;
Matches 353; Conservative 53; Mismatches 153; Indels 13; Gaps 3;

QY 9 LTPLELLLSMLLLGTRPHGSPGLQCYSGVPLGLNCSWEPLGDLTPPPVLYHQSQKY 68
DB 14 lpklaillplwlfgrtrpqgsagplqcyvgplgdlncsweplgdlgapshelhqsky 73
QY 69 HPNRWEVKVPKSKQSWITPRQFTMADKLLIWGTQKGRPLWSSVSNLETKMPTPOI 128
DB 74 rsnktqtvaagrsawaipreqlmsdkllwvqkagqplwppvfvnletgmknapi 133
QY 129 FSQVDISEATLEATVQWAPPVWPQKALTCQFRYKECAEAWTRLEPOLKTDGTPVEM 188
DB 134 gpdvfdsedpdeatvhwappwpskhvliqcfryrqcaawtllpeelktiptpei 193
QY 189 QNLEPGTCYQVSGRCQVGENYP-WGEWSSPLSFQTFPFLDPEDVWVSGTVCETSGRAALL 247
DB 194 qdeleatgykyvgrcrmekeedlwgepslilsfqtppsapkdvwvsgnlcgtppgeep 253
QY 248 VMDPRPCVQVITYVWFGAGDITTTQEEVPCKSPVPAWMEWAVSPGNSTSWVPPTNLS 307
DB 254 lwkagpcvqvykvwfwvgrrelspegitccclipsgaeavrsavnatsewptnls 313
QY 308 LVCLAPESAPCDVGVSSADGSPGIKVTWKQGRKPLEYVVDWAQDGLSKLWTRLPVEM 367
DB 314 lvcldsaaprsvavssilagsteillvtwqpggeplehvmwdardgplekinwrlppg 373
QY 368 NLSTLLPGFEKGGVPYRTVTAVYSGGLAAAPSVWGFREELVPLAGPAVWRLPDDPPGTP 427
DB 374 nlsallpgnftvgvpyriltvavssaglasavsvwgfrelaplvgtlwrldqappgcp 433
QY 428 VYAWGEVPRHQRLQGATHYTFICIQSRGLSTVCRNVSSQTQTATLPNLHSGSFKLWTVST 487
DB 434 alawgevrhqlrghlthyltcaqgstpsvcmvsgntqstvtlpldwpgpcelwvtast 493
QY 488 VAGQPGPGDLSHLPLDNRIRKALPWFILSLWGLLWGLLWGLSLASTRCLQARCLHWRHKL 547
DB 494 laggpgppilrhipdntlrwkvlpglflwglfllgclslats----grcyhlrhkv 549
QY 548 LPQWIERVPDPANSSNGOPYIKVSLPQPKDGPILVEEVELOPVVES---PKASAPI 604
DB 550 lprwwekvpdpansssgqphmeqvpeaqplgdplileveempppvmeassqagatapi 609
```



CC innate immunity and/or morphogenic development. (R), antibodies and  
CC ligands are useful for treatment of conditions, especially immunological  
CC disorders, associated with conditions exhibiting abnormal expression of  
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
CC and the subunits DSR1 and DCR1 are useful as immunogens for generating  
CC antibodies, or as antigens for binding antibodies. Nucleic acids  
CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
CC variants from other individuals or species. The present sequence  
CC represents the partial mouse DCR1, given in the present invention.  
XX  
SQ Sequence 246 AA;

Query Match 39.2%; Score 1342; DB 20; Length 246;  
Best Local Similarity 100.0%; Pred. No. 2.3e-99;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 378 KGVPRYRTVAVYSGGLAAASVGVFRELYVPLAGPAWRPLDDPGTPVVAWGEVPRH 437  
D 1 kggvpyritvtavysgglaaapsvvgfreelyvplagpavwripddpgtpvvaawgevprh 60  
QY 438 QLRGQATHYFCIQRGSLSTVCVRNYSSTQTATPLNLHSGFKLVTVSTVAGQGPDPD 497  
D 61 qlrgqathyfcicqrgslstvcvrnysvsgtqatplnlhsgsfklwvstvsgqgppgpd 120  
QY 498 LSLHLPDNRIRKALPWFUSLWGLLMLGCLSLASTRCLOARCLHWRHKLPLQWIWERYP 557  
D 121 lslhlpdnrirkalpwwfslwglmlgclslastrclqarclhwrhklplqwiewervp 180  
QY 558 DPANNSGGPYIKEVSLPPDKGPILVEVEVELQPVVSPKASAPIYSGYKHFPTPE 617  
D 181 dpannsqgpyikevslppdkdgpilveeveelqpvvespkasapiysgyekhflptpe 240  
QY 618 ELGLLV 623  
D 241 elgllv 246

RESULT 9  
ID AAY29782  
XX AAY29782 standard; Protein; 150 AA.  
AC AAY29782;  
XX  
DT 04-NOV-1999 (first entry)  
XX  
DE Mouse DNAX cytokine receptor subunit 1.  
XX  
KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
KW Interleukin B30; DSR1; DCR1; IL-B30; cytokine receptor; diagnosis;  
KW inflammatory disorder; inflammatory response; innate immunity;  
KW morphogenic development; immunological disorder.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 150  
FT /label= unknown  
FT /note= "encoded by GAN"  
XX  
PN WO9940195-A1.  
XX  
PD 12-AUG-1999.  
XX  
PF 05-FEB-1999; 99WO-US02600.  
XX  
PR 13-MAY-1998; 98US-0078194.  
PR 06-FEB-1998; 98US-0073941.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Kastelein RA, Mattson JD, McManahan TK;

DR WPI; 1999-527306/44.  
DR N-PSDB; AAZ08864.  
XX  
PT New receptor subunits useful in the treatment inflammatory disorders  
XX  
PS Claim 2; Page 17-18; 133pp; English.  
XX  
CC The present invention describes a composition (I) comprising DNAX  
CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
CC subunit I (DSRS1) protein, which together encode a new mammalian  
CC cytokine-related receptor (R), or DCR1 and interleukin B30 (IL-B30)  
CC proteins, or DSR1 and IL-B30 proteins. (I) comprising DSR1 and DCR1  
CC is useful for screening for ligands (i.e. agonists/antagonists) from  
CC a library of compounds, which are useful for modulating the physiology  
CC or development of a cell or tissue culture e.g. inflammatory responses,  
CC innate immunity and/or morphogenic development. (R), antibodies and  
CC ligands are useful for treatment of conditions, especially immunological  
CC disorders, associated with conditions exhibiting abnormal expression of  
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
CC and the subunits DSR1 and DCR1 are useful as immunogens for generating  
CC antibodies, or as antigens for binding antibodies. Nucleic acids  
CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
CC variants from other individuals or species. The present sequence  
CC represents the specifically claimed mouse DCR1, for use in the  
CC composition of the present invention.  
XX  
SQ Sequence 150 AA;  
XX  
Query Match 20.8%; Score 712; DB 20; Length 150;  
Best Local Similarity 98.5%; Pred. No. 2.7e-49;  
Matches 133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MNRLRVARLTPLLELLSLMSLLGTRPHGSPGLQCYSGVPLGILMCSWEPLDLETPPV 60  
D 15 mnrifgarltpllellslmslllgttrphgspglqcyvgplilncswepldletppv 74  
QY 61 LYHQSQKYHPNRVWEVKVPSKOSWVTIPREQFTMAKLLIWTQKGRPLMSSVSVNLETQ 120  
D 75 lyhqsqkyhpnrvwevkvpkqswvtipreqftmadklllwtqkgrplwssvsvnletq 134  
QY 121 MKPDTPOIFSOVDIS 135  
D 135 mkpdtppqifsqvdls 149  
XX  
RESULT 10  
AAW12771  
ID AAW12771 standard; Protein; 862 AA.  
XX  
AC AAW12771;  
XX  
DT 12-MAY-1997 (first entry)  
XX  
DE Human interleukin-12 beta-2 receptor.  
XX  
KW Interleukin-12 beta-2 receptor; IL-12; autoimmune disease;  
KW rheumatoid arthritis; inflammatory bowel disease;  
KW multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= Sig\_peptide  
FT Domain 24..622  
FT /label= Extracellular\_domain  
FT Domain 623..646  
FT /label= Transmembrane\_domain  
FT Domain 647..862  
FT /label= Cytoplasmic\_tail  
FT Region 132..145  
FT /label= Cytokine\_receptor\_motif





FT Protein 45..1001 /label Mature\_peptide

XX WO9210570-A.

XX 25-JUN-1992.

XX 05-DEC-1991; 91WO-US09112.

XX 13-DEC-1990; 90US-0626725.

XX 13-MAR-1991; 91US-0670608.

XX (IMMV ) IMMUNEX CORP.

XX Beckmann MP, Gearing DP;

XX WPI: 1992-234626/28.

XX N-PSDB; AAQ25799.

XX New leukaemia inhibitory factor receptor proteins - for treating

XX LIF-dependent leukaemia, lipoprotein, bone and calcium metabolism

XX defects e.g. atherosclerosis, obesity etc.

XX Disclosure: Page 28-32; 49pp; English.

XX The sequence given is a leukemia inhibitory factor (LIF)-receptor

XX (LIF-R). LIF-R proteins are present on the surface of various

XX hematopoietic and non-hematopoietic cells. They are capable of

XX binding LIF molecules. They are mammalian plasma membrane proteins

XX and play an important role in transducing the signal provided by LIF

XX to a cell. This protein has a molecular weight of approx. 190,000 kD.

XX LIF-R proteins can be used to competitively bind LIF and thereby

XX inhibit its binding to cell surface receptors. Soluble LIF-R may be

XX used in therapy to inhibit the effects of LIF-induced cachexia in

XX cancer patients to treat lipoprotein metabolism defects such as

XX atherosclerosis and obesity. It may also be useful in the treatment

XX of disorders of bone and calcium metabolism or disorders associated

XX with LIF overproduction associated with hepatocytes, neurons and

XX leukocytes.

XX Sequence 1001 AA;

Query Match 8.2%; Score 280; DB 13; Length 1001;

Best Local Similarity 21.5%; Pred. No. 1.2e-13;

Matches 142; Conservative 110; Mismatches 264; Indels 144; Gaps 35;

QY 27 PHGSPGLOQYSGVPLGILNCSWEP-----LGDLETPPVLYHQ-SQKYHPNRVWEVKVP 79

DB 332 pPdtPqqlnc-ethdikeilcswmrvrtalvgpratsytlvestsgky--vrlkraeap 388

QY 80 SKQSW---VTIPREQ---FTWADKLLIWGTQGRPL---WSVSVNLETQMKPDPQPQIF 129

DB 389 tnesyqlfcmipnqenynftl-----nahmplgrsqstiltvntekvyphtptsf 439

QY 130 SQVDISEATLEATVQMAPVPVWPPKQALTCQFRYKCOQAEAWTRLEPQLKTDGLTP---- 185

DB 440 kvkdlnsta---vklswhlpgnfakinficeileiknsn---vqeqrvntikigvessyl 493

QY 186 VEMQNLEPCTCQVSGRCQVENCYPKGENSSPLSFQTPFLDPE---DVMVSGTVGCTSGK 242

DB 494 valdklnpytlyfrircstetfsvkswsknkkhlitteespskgpdtv-----rewssd 548

QY 243 RAALLWKPDPFCVQ-----VVTYVWFAGDITTTQEEVPCCKSPVPANWE-----WAVV 292

DB 549 gknllyskplpneangkilysnvscsdeetqslseipdpqhkaqrlidkndyilsvv 608

QY 293 SPGNSTSWVPNTNLVLCLAPESAPCDVGVSSADG-SPGKVTWKQGRKRPLEYVVDMAQ 351

DB 609 ak-nsvgssppskia-----smeipnddlkieqvvgmgkgilltnhdydpmtcdyikwsn 663

QY 352 DGDSDLKL-NWTRLPGNLSTLLFG-EFKGGVPYRITVTAVYSGGLAAPSVWGFREELY 409

Db 664 ssrsepclmdwtkvpsnstetviesdefrpglrynflygrnngyqlrlrmigyleela 723

QY 410 PLAGPAVWRLLPDDPGTPVYVAMGEVPRHQLRGQATHVTF-----CQSRGLS 456

Db 724 pivapn-ftvedtsadslvkwedipveelrgrflrlyfyfkgkgrdtksmrviessrsd 782

QY 457 TVCRNVSSQTO-TATLNLH-SGSFKLWTVTVAGQPPGDLSUHL--PDNRIRWKAL 512

Db 783 ikvknitdisqktlriadiqgktsyhlvrayt---dggvgpeksmvvyvckensv----- 834

QY 513 PWFSLWGLL-----LMCGGLSLASTRCQARCLHWRHKLPLQWIWER----VP 557

Db 835 -----gllailipvavavivg---vtsilcykr-----ewiketfypdip 874

QY 558 DPANSNS-----GQPIKVEVSL-PQPPKDGPILE-----VVEVF-LQPVVESPK 599

Db 875 npenckalqfksvcegsaalkleinpctpnnvletrsaafpkiedtelispaerpe 934

RESULT 12

AAQ49508

ID AAR49508 standard; Protein; 1097 AA.

XX AAR49508;

XX 07-JUL-1994 (first entry)

XX Human LIF-R.

KW LIF-R; leukemia inhibitory factor receptor.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..44

FT Domain 1..789 /label Sig\_peptide

FT Region 790..815 /label Extracellular\_domain

FT Domain 816..1054 /label Transmembrane\_region

FT Domain /label Cytoplasmic\_domain

XX US5284755-A.

XX 08-FEB-1994.

XX 13-DEC-1990; 90US-0626725.

XX 13-DEC-1990; 90US-0626725.

XX 13-MAR-1991; 91US-0670608.

XX 11-SEP-1992; 92US-0943843.

XX (IMMV ) IMMUNEX CORP.

XX Beckmann MP, Gearing DP;

XX WPI: 1994-056341/07.

XX N-PSDB; AAQ58427.

XX DNA encoding leukaemia inhibitory factor receptor - esp. soluble

XX receptor, used as competitive inhibitor of LIF binding to cell

XX surface, in therapy, diagnosis and assays

XX Disclosure: Column 63-64 to 69-70; 44pp; English.

XX Plasmid pHIFR-65 (ATCC 68491) includes human placental LIF-R cDNA

XX (given in AAQ58425) encoding a C-terminal truncated LIF-R protein

XX (AAQ49506). Screening of human cDNA and genomic libraries using this

XX cDNA yielded composite sequence AAQ58427 encoding full-length human

XX LIF-R (AAQ49508). cDNA of sequence AAQ58426, encoding mouse LIF-R

XX (AAQ49507), was obtained by screening a liver cDNA library with a human

XX LIF-R probe. A soluble human LIF-R/Fc homodimer can be prepared

CC using sequence AAQ58428 encoding protein AAR49509.

XX Sequence 1097 AA;

Query Match 8.1%; Score 277; DB 15; Length 1097;

Best Local Similarity 21.7%; Pred. No. 2.5e-13;

Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

Qy 27 PHGSPGLQCYSVGLGLNCSWEP-----LGDLTPPVLYHQ-SQKYHPNRVWEKVP 79

Db 332 pddtqqqlnc-ethldkciicswpgprvtalvgpratsytivesfsgky--vrlkraap 388

Qy 80 SKQSH-----VTIPRQ-----FTMADKLLIWGTQGRPL---WSSVSNLETKMKTPTQIF 129

Db 389 tnesyqlilfqlmqlpndeifnftl-----nahnpgrsgstlilvntekvyphptstf 439

Qy 130 SOVDISEATLENTVQWAPPVPPQKALTCQRYKECAEAWTRLEPQLKTDGLTP---- 185

Db 440 kvkdlnsta---vklshlpgnfafinfclelelkkns---vqeqrnvtikgvnsyl 493

Qy 186 VEMQLEPCTCYQVSGRCQVNGYVWGWSSPLSFQTPFLDPE---DVWVSGTVCETSGK 242

Db 494 valdklnpytlytfircstetfkwskwnkkqlhtteaspskpdtrwews---sdgk 550

Qy 243 RAALLVWKDPRCQVQ-----VYTVWFGAGDITTTQEEVPCKSPVPAWME-----WAVY 292

Db 551 n-liiywk-pipineangkilsynvscsdeetqslseipdpqhkaeirlkndyilsvv 608

Qy 293 SPGNSTSVPTNLVLCLAPESAPCDVGVSSADG-SPGIKVTWKQGTREKPLEYVVDNAQ 351

Db 609 ak-nsvgsppskia-----smelpnddlikiegvmgkgliltwhypnmtcdyvikwcn 663

Qy 352 DGDSDKL-NWTRLPPLGNSLTLLPG-ERKGGVPRITVTAVVSGGLAAAPSVMGFREELV 409

Db 664 srspeclmdwrkpsnstetviesdefpgrirynfflygrngqyqlrlsmigyeela 723

Qy 410 PLAGPAVWRLPDDPGTPPVAVGEVPRHQLRGQATHYTF-----CIGSRGLS 456

Db 724 pivapn-ftvedtsadsilvkwedipveelrgflrgyifgkgerdtskmrvlesgrsd 782

Qy 457 TVCRNVSSQTC-TATLPNLH-SGSFKLWTVSTVAGQPGPDLSLHL--PDNRIRWAL 512

Db 783 lkvknitdisqktriadlqgktyhvirayt---dggvgpeksmyvvtkensv----- 834

Qy 513 PWFSLMGLL-----LMGGLSLASTRCLOARCLHWRHKLDPQWTWER-----VP 557

Db 835 -----glialilipvavivgv---vtsilcykr-----ewiketfypdip 874

Qy 558 DPANSNS-----GQPYIKEVSL-POPPKDGPILE-----VEEVE-LQPVVESP 599

Db 875 npencalqfksvecgssalktlempnctpnnevletrsafpkiedtelispvaepr 934

RESULT 13

AAR45776

ID AAR45776 standard; Protein; 1097 AA.

XX AC AAR45776;

XX AC AAR45776;

DT 04-AUG-1994 (first entry)

DE Human leukaemia inhibitory factor receptor (clone hulifr.65-gen).

KW Leukaemia inhibitory factor receptor; LIFR; LIF; therapy;

KW diagnosis; assay; antibodies; inhibition; cachexia;

KW atherosclerosis; obesity; bone; calcium; metabolism.

XX OS Homo sapiens.

XX OS Homo sapiens.

FT Key Location/Qualifiers

FT Region 1..44

FT /label= Signal peptide.

FT Peptide 45..1097  
FT /label= Mature peptide.  
FT 55 /note= "Hallmark residue associated with the  
FT haematopoietin family of receptors."  
FT Modified-site  
FT Region  
FT 64 /note= "Potential N-linked glycosylation site."  
FT 65 /note= "Hallmark residue associated with the  
FT haematopoietin family of receptors."  
FT Region  
FT 82 /note= "Hallmark residue associated with the  
FT haematopoietin family of receptors."  
FT Modified-site  
FT Region  
FT 85 /note= "Potential N-linked glycosylation site."  
FT 90 /note= "Hallmark residue associated with the  
FT haematopoietin family of receptors."  
FT Modified-site  
FT Region  
FT 131 /note= "Potential N-linked glycosylation site."  
FT 143 /note= "Potential N-linked glycosylation site."  
FT 191 /note= "Potential N-linked glycosylation site."  
FT 235..236 /note= "Potential N-linked glycosylation site."  
FT /note= "Hallmark residue associated with the  
FT haematopoietin family of receptors."  
FT 238..239 /note= "Hallmark residue associated with the  
FT haematopoietin family of receptors."  
FT Modified-site  
FT Region  
FT 243 /note= "Potential N-linked glycosylation site."  
FT 303 /note= "Potential N-linked glycosylation site."  
FT 341 /note= "Hallmark residue associated with the  
FT haematopoietin family of receptors."  
FT Region  
FT 351 /note= "Hallmark residue associated with the  
FT haematopoietin family of receptors."  
FT Modified-site  
FT Region  
FT 390 /note= "Potential N-linked glycosylation site."  
FT 407 /note= "Potential N-linked glycosylation site."  
FT 426 /note= "Potential N-linked glycosylation site."  
FT 445 /note= "Potential N-linked glycosylation site."  
FT 481 /note= "Potential N-linked glycosylation site."  
FT 489 /note= "Potential N-linked glycosylation site."  
FT 519..520 /note= "Potential N-linked glycosylation site."  
FT /note= "Hallmark residue associated with the  
FT haematopoietin family of receptors."  
FT 522..523 /note= "Hallmark residue associated with the  
FT haematopoietin family of receptors."  
FT Modified-site  
FT Region  
FT 572 /note= "Potential N-linked glycosylation site."  
FT 652 /note= "Potential N-linked glycosylation site."  
FT 663 /note= "Potential N-linked glycosylation site."  
FT 680 /note= "Potential N-linked glycosylation site."  
FT 729 /note= "Potential N-linked glycosylation site."  
FT 787 /note= "Potential N-linked glycosylation site."  
FT 834..859 /note= "Potential N-linked glycosylation site."  
FT /label= Transmembrane domain.  
FT 1010 Modified-site



FT Modified-site 729 /note= "glycosylation site"  
 FT Modified-site 787 /note= "glycosylation site"  
 FT Domain 834..859 /note= "transmembrane domain"  
 FT Modified-site 1010 /note= "glycosylation site"  
 FT US5420247-A.  
 XX 30-MAY-1995.  
 XX 13-DEC-1990; 90US-0626725.  
 XX 11-SEP-1992; 92US-0943843.  
 PR 13-DEC-1990; 90US-0626725.  
 PR 13-MAR-1991; 91US-0670608.  
 XX (IMMV ) IMMUNEX CORP.  
 PA Beckmann PM, Gearing DP;  
 XX WPI: 1995-206309/27.  
 DR N-PSDB; AAQ92272.  
 XX New leukaemia inhibitory factor receptor proteins - useful for  
 PT research, therapeutic and diagnostic purposes, esp. for the  
 PT treatment of cancer associated cachexia  
 PT Claim 1; Column 57-64; 47pp; English.  
 PS This sequence represents human leukaemia inhibitory factor receptor  
 XX (LIF-R). This sequence was encoded by the composite full length cDNA  
 CC for human LIF-R. The cDNA sequence was isolated by screening human cDNA  
 CC and genomic libraries with a probe derived from human clone 65 LIF-R  
 CC cDNA. This receptor mediates LIF activity. LIF is a polypeptide hormone  
 CC which acts on a variety of cells, and is highly conserved in a variety  
 CC of species. LIF-R is present on the surface of a large number of  
 CC hematopoietic and non-hematopoietic cells, including monocyte  
 CC macrophages, megakaryocytes, osteoblasts and placental trophoblasts.  
 CC The proteins represented by AAR74095-6 are also LIF-R proteins. These  
 CC proteins are useful for research, where they can be used to study the  
 CC structural and biological characteristics of native LIF-R. They are also  
 CC useful for therapeutic purposes, e.g. to treat cachexia, atherosclerosis,  
 CC obesity or bone disorders, and can be used for diagnostic purposes, e.g.  
 CC for determination of LIF or diagnosis of diseases associated with  
 CC abnormal LIF-R.  
 XX Sequence 1097 AA;  
 S Query Match 8.1%; Score 277; DB 16; Length 1097;  
 Best Local Similarity 21.7%; Pred. No. 2,5e-13;  
 Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;  
 QY 27 PHGSPGLQCYSGVGLILNCWEP-----LGDLETPPVLYHQ-SQKYHPNRVMEVKVP 79  
 DB 332 pddtpqqlnc-ethdlkeilcswnpgrvtalvgpratsyltvesfsgky--vrikraeap 388  
 QY 80 SKQSW----VTIPREQ---FTMADKLLIWGTQGRPL---WSSVSVNLETKMKTPTQIF 129  
 DB 389 tnesyqlfqlmnpqelynftl-----nahnplgrsgstlilvntekvyphptpsf 439  
 QY 130 SQVDISEATLEATVQWAPPVWPQKALTCQFRVKEQAEAWTRLEPQLKTDGLTP---- 185  
 DB 440 kvkdinsta----vklshlpgnfakinfleieikns----vdeqrnvtlkgvenssyl 493  
 QY 186 VEMONLEPPTCYQVSGRCQVENGYPWGEWSPLSFOTPFILDPE---DWVSGTVCEISGK 242  
 DB 494 valdklapytlytfricrstetfkwskwnkqhlteaspskgpdtwrews---sdgk 550  
 QY 243 RAALLVWKDRPCVQ-----VTTYTWFGAGDITTTQEBVPCCKSPVPANMB-----NAWV 292

Db 551 n-liiywk-pipineangkilsynvscsdeetqtsiseipdqghkaeifrlkndyisvv 608  
 QY 293 SPGNSTSNVPTNLNLVCLAPESAPCDGVSSADG-SPGKIKVTWKGTRKPLEYVVDWAQ 351  
 Db 609 ak-nsvgsppskia-----smelpnddikiqevvgmgkglllltwhydpmtcdyvikwn 663  
 QY 352 DGDSDLKL-NWTRLPPGNLSTLLPG-EFKGGVPIRYITVAVYSGGLAAAPSVMGFPREELV 409  
 Db 664 srssepclmdwrkvpnsstetviesdefrgirynfflygcrrnqgqllrsmigyleela 723  
 QY 410 PLAGPAVWRLPDDPGTPVWANGEVPRHQLRQATHYTF-----CIGRGLS 456  
 Db 724 pivapn-ftvedtsadslivkwedipvealrgflgyfkgkgerdtakmrvesgrsd 782  
 QY 457 TVCRNVSSQTO-TATLPNLH-SGSFKLWTVSTVAGQPPGPDLSLHL--PDNRIRWKAL 512  
 Db 783 lkvknitdisqkltliadiqgktsyhlvirayt---dggvgpeksmyvvtkensk----- 834  
 QY 513 PMFLSLWGLL-----LMGCGLSLASTRCLOARCLHWRHKLKPQWIWER-----VP 557  
 Db 835 -----gliitailipvavavivgv---vtsilcykr-----ewiketfypdip 874  
 QY 558 DPANSNS-----GQPIYKEVSL-POPPKDGPILE-----VEEVE-LQPVVESP 599  
 Db 875 npenckalqfksvcegsalktlempctpnnevletrsafpkiedteifspvaerpe 934  
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 AAR45774  
 ID AAR45774 standard; Protein; 1001 AA.  
 XX AAR45774;  
 XX AC AAR45774;  
 XX DT 04-AUG-1994 (first entry)  
 XX DE Human leukaemia inhibitory factor receptor (clone hulifr.65).  
 XX KW Leukaemia inhibitory factor receptor; LIFR; LIF; therapy;  
 KW diagnosis; assay; antibodies; inhibition; cachexia;  
 KW atherosclerosis; obesity; bone; calcium; metabolism.  
 XX OS Homo sapiens.  
 XX PN US284755-A.  
 XX PD 08-FEB-1994.  
 XX PF 13-DEC-1990; 90US-0626725.  
 XX PR 13-DEC-1990; 90US-0626725.  
 PR 13-MAR-1991; 91US-0670608.  
 PR 11-SEP-1992; 92US-0943843.  
 XX (IMMV ) IMMUNEX CORP.  
 XX Beckmann MP, Gearing DP;  
 XX WPI: 1994-056341/07.  
 DR N-PSDB; AAQ55940.  
 XX DNA encoding leukaemia inhibitory factor receptor - esp. soluble  
 PT receptor, used as competitive inhibitor of LIF binding to cell  
 PT surface, in therapy, diagnosis and assays  
 XX Claim 1; Column 42-48; 44pp; English.  
 XX Soluble forms of the leukaemia inhibitory factor receptor (LIFR)  
 CC having the transmembrane domain deleted can be used in therapy,  
 CC diagnosis, in assays for LIF or LIFR, or for raising antibodies to  
 CC LIFR. Soluble LIFR proteins can be used for competitive inhibition  
 CC of binding of LIF to cell surface receptors. Conditions which could  
 CC benefit from such inhibition include LIF-induced cachexia in cancer

CC patients and lipoprotein metabolism disorders such as  
 CC atherosclerosis and obesity. Soluble LIFR is also useful in the  
 CC treatment of disorders of bone and calcium metabolism as well as  
 CC those associated with the over production of LIF in e.g.  
 CC hepatocytes, neurons and leukocytes. The LIFR clone 65 is a 5'  
 CC fragment lacking the 3' end.

XX  
 SQ Sequence 1001 AA;

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Query Match      8.1%; Score 276; DB 15; Length 1001;
Best Local Similarity 21.7%; Pred. No. 2.6e-13;
Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

QY 27 PHGSGPLQCYSGVGLIINCWEP-----LGDLETPPVLYHQ-SQKYHPNVRVWEVKVP 79
DB 332 pddtqqlnc-ethdlkeicawnpgrvtalvgpratsylvesfsgky--vrlkraeap 388
QY 80 SKQSW---VTIPREQ---FTMADKLLINGTQKGRPL---WSSVSYNLETKMKPDPPIQIF 129
DB 389 tnesyqllfqmlpnqeiynftl-----nahnpigrsqstiltvntekevyphtptsf 439
QY 130 SQVDISEATLEATVQWAPVPPQKALTCQPRYKCEQAEATRLPEQLKTDGLTP----- 185
DB 440 kvkdlnta---vklshlpgnfakinficeiteikksns---vqedrntvikgvenssyl 493
QY 186 VEMQNLEPGTCYQVSGRCOVENGYPMGEWSSPLSFOTPFLDPE---DVWVSGTVCTSGK 242
DB 494 valdklnpytlyfrircstetfkwskwnnkqhltteaspskgpdtwreus---sdgk 550
QY 243 RAALLVWKDPRPCVQ-----VYTYVWFGADITTTQEEVPCCKSPVPANME-----WAVV 292
DB 551 n-lilywk-plpineangkilsynvscsdeetqslseipdpqhkaeirldkndyivsvv 608
QY 293 SPGNSTSWVPPTNLSVLCLAPESAPCDVGVSSADG-SPGIKVTWKQGTAKPLEYVVDWAQ 351
DB 609 ak-nsvgsppakia-----smeipnddlkieqvvgmgkgllitwhypnmtcdyvikwn 663
QY 352 DGDSDLKL-NWTRLPGNLSLTPG-EFRKGVYPYRTTAVYSGGLAAAPSVMGFPREELV 409
DB 664 srssepclmdwrvkpanstetviesdefpgirynfflygcrnqgyqlrsmigyieela 723
QY 410 PLAGPAVWRLPDDPGTTPVAVNGEVRPHRLRGOATHYTF-----CIGSRGLS 456
DB 724 pivapn-ftvedtsadsilvkwedipveelrgflrylyfgkgerdtskrmrvlesgrsd 782
QY 457 TVCRNVSSQTO-TATLPNLH-SGSFKLWTVTVAGQGPDPDLSLHL--PDNRIWKAL 512
DB 783 ikvknitdisqkrlriadiqgktsyhlvrayt---dggvgpkeksmyvvtkensv----- 834
QY 513 PWFLSLWGLL-----LMGCGLSUASTRCQLQARCLHWRHKLKPQIWER-----Vp 557
DB 835 -----gliaillpvavavivqv---vtsilcyzkr-----ewiketfypdip 874
QY 558 DPANSNS-----GQPYIKEVSL-PQPPKDGPILE-----VEEVE-LQPVVESPK 599
DB 875 npenckalqfksvcgssalktlempnctpnnveletrsafpkiedteilspsvaerpe 934

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Search completed: May 9, 2002, 06:06:16  
 Job time: 148 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2002, 06:04:24 ; Search time 24.01 Seconds  
(without alignments)  
583.905 Million cell updates/sec

Title: US-09-692-504-2  
Perfect score: 3424  
Sequence: 1 MNRLRVARLTPELLLSLMS.....IYSGYEKHFPTPEELGLLV 623

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues  
number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3424	100.0	623	1	US-08-653-740-7
2	3424	100.0	623	2	US-09-073-594-7
3	3424	100.0	623	3	US-09-275-925-7
4	2044	59.7	636	1	US-08-653-740-5
5	2044	59.7	636	2	US-09-073-594-5
6	2044	59.7	636	3	US-09-275-925-5
7	1866.5	54.5	578	1	US-08-653-740-3
8	1866.5	54.5	578	2	US-09-073-594-3
9	1866.5	54.5	578	3	US-09-275-925-3
10	384	11.2	862	2	US-08-685-118-2
11	384	11.2	862	2	US-08-915-495-2
12	384	11.2	862	2	US-08-914-520-2
13	277	8.1	620	2	US-08-419-652-7
14	277	8.1	1001	1	US-07-797-556-6
15	277	8.1	1001	1	US-07-943-843-2
16	277	8.1	1001	1	US-08-347-003-2
17	277	8.1	1097	1	US-07-943-843-6
18	277	8.1	1097	1	US-08-347-003-6
19	270	7.9	708	1	US-07-797-556-2
20	270	7.9	708	1	US-08-308-881-2
21	270	7.9	708	2	US-09-058-263-2
22	270	7.9	708	2	US-09-059-099-2
23	270	7.9	708	3	US-09-058-264-2
24	270	7.9	708	5	PCT-US95-06530-2
25	264	7.7	918	2	US-08-825-558-6
26	261	7.6	602	2	US-08-419-652-6
27	261	7.6	783	6	5422248-2

28	261	7.6	836	1	US-07-923-976-4	Sequence 4, Appl1
29	255.5	7.5	837	1	US-07-923-976-2	Sequence 2, Appl1
30	253	7.4	572	2	US-08-419-652-5	Sequence 5, Appl1
31	253	7.4	863	1	US-07-923-976-8	Sequence 8, Appl1
32	228	6.7	771	1	US-07-923-976-6	Sequence 6, Appl1
33	226	6.6	658	2	US-08-825-558-4	Sequence 4, Appl1
34	193.5	5.7	979	1	US-08-308-881-6	Sequence 6, Appl1
35	193.5	5.7	979	2	US-09-058-263-6	Sequence 6, Appl1
36	193.5	5.7	979	3	US-09-059-099-6	Sequence 6, Appl1
37	193.5	5.7	979	3	US-09-058-264-6	Sequence 6, Appl1
38	193.5	5.7	979	5	PCT-US95-06530-6	Sequence 6, Appl1
39	176.5	5.2	719	1	US-07-943-843-4	Sequence 4, Appl1
40	176.5	5.2	719	1	US-08-347-003-4	Sequence 4, Appl1
41	175	5.1	488	2	US-08-599-455B-5	Sequence 5, Appl1
42	175	5.1	488	4	US-09-069-781B-5	Sequence 5, Appl1
43	153	4.5	894	2	US-08-599-455B-2	Sequence 2, Appl1
44	153	4.5	894	4	US-09-069-781B-2	Sequence 2, Appl1
45	153	4.5	896	2	US-08-640-389A-12	Sequence 12, Appl1

ALIGNMENTS

RESULT 1  
US-08-653-740-7  
; Sequence 7, Application US/08653740  
; Patent No. 5792850  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/653,740  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 623 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-653-740-7

Query Match 100.0%; Score 3424; DB 1; Length 623;  
Best Local Similarity 100.0%; Pred. No. 3e+292;  
Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNRLRVARLTPELLLSLMSLLGTRPHGSPGLOCYSVGPGLGILNCSEWPLGLDLETPPV 60  
Db 1 MNRLRVARLTPELLLSLMSLLGTRPHGSPGLOCYSVGPGLGILNCSEWPLGLDLETPPV 60





ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-31  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 623 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-275-925-7

Query Match 100.0%; Score 3424; DB 3; Length 623;  
Best Local Similarity 100.0%; Pred. No. 3e-292;  
Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRRLVARLTPLLELLLSMLLLGTRPHGSPGLQCYSGVPLGILNCSWEPLGDLTPPV 60  
DB 1 MNRRLVARLTPLLELLLSMLLLGTRPHGSPGLQCYSGVPLGILNCSWEPLGDLTPPV 60  
QY 61 LYHQSKYHPNRVWVKVPSQSWTIPREQFTMDKLLINGTKGRPLWSSVSNLETO 120  
DB 61 LYHQSKYHPNRVWVKVPSQSWTIPREQFTMDKLLINGTKGRPLWSSVSNLETO 120  
QY 121 MKPDPPIFSQVDISEATLEATVQWAPPVMPQKALTCQFRYKCEQAEAWTRLEPQKT 180  
DB 121 MKPDPPIFSQVDISEATLEATVQWAPPVMPQKALTCQFRYKCEQAEAWTRLEPQKT 180  
QY 181 DGLTPVENQNLPGTCYQVSGRCQVNGYPMGWSPLSFQTPFLDPEDVWVSGTVCE 240  
DB 181 DGLTPVENQNLPGTCYQVSGRCQVNGYPMGWSPLSFQTPFLDPEDVWVSGTVCE 240  
QY 241 GKRAALLVWKDPRPCVQVYTWFGAGDITTTQEEVPCKSPVPAMWMAVVSNGNSTSW 300  
DB 241 GKRAALLVWKDPRPCVQVYTWFGAGDITTTQEEVPCKSPVPAMWMAVVSNGNSTSW 300  
QY 301 VPPTNLSLVCLAPESAPCDVGVSSADSGPGIKVTWKQTRKPLEYVVDWAQDGSIDLK 360  
DB 301 VPPTNLSLVCLAPESAPCDVGVSSADSGPGIKVTWKQTRKPLEYVVDWAQDGSIDLK 360  
QY 361 WTRLPNGNLSTLLPGEFGGVPYRITVAVYSGGLAAAPSVMGFREELVPLAGPAWRLP 420  
DB 361 WTRLPNGNLSTLLPGEFGGVPYRITVAVYSGGLAAAPSVMGFREELVPLAGPAWRLP 420  
QY 421 DPPGTPVWVAMEVPRHQLRGQATHYTFICQSRGLSTVCRNVSSOTQATLPLNLSGSE 480  
DB 421 DPPGTPVWVAMEVPRHQLRGQATHYTFICQSRGLSTVCRNVSSOTQATLPLNLSGSE 480  
QY 481 LWVTVSTVAGQPPGPDLSLPLDNRIWKALPWFSLWGLLMLGCLSLASTRCLQARC 540  
DB 481 LWVTVSTVAGQPPGPDLSLPLDNRIWKALPWFSLWGLLMLGCLSLASTRCLQARC 540  
QY 541 LHWHRKLLPQWIWVRPDPANSQGYIKEYVSLPQPKDGPILVEVEVELOPVVSPKA 600  
DB 541 LHWHRKLLPQWIWVRPDPANSQGYIKEYVSLPQPKDGPILVEVEVELOPVVSPKA 600

DB 541 LHWHRKLLPQWIWVRPDPANSQGYIKEYVSLPQPKDGPILVEVEVELOPVVSPKA 600  
QY 601 SAPIYSGYEKHEFLPTPEELGLLV 623  
DB 601 SAPIYSGYEKHEFLPTPEELGLLV 623

RESULT 4  
US-08-653-740-5  
Sequence 5, Application US/08653740  
Patent No. 5792850  
GENERAL INFORMATION:  
APPLICANT: James W. Baumgartner  
APPLICANT: Donald C. Foster  
APPLICANT: Frank J. Grant  
APPLICANT: Cindy A. Sprecher  
TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/653,740  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 636 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-653-740-5

Query Match 59.7%; Score 2044; DB 1; Length 636;  
Best Local Similarity 62.8%; Pred. No. 4.4e-171;  
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

QY 9 LTPLELLLSMLLLGTRPHGSPGLQCYSGVPLGILNCSWEPLGDLTPPVLYHQSKY 68  
DB 14 LPKLALLPLLWLLFQTRPQSGAGPLQCYGVGPLGDLNCSWEPLGDLGAPSLHLQSKY 73  
QY 69 HPNRVWVKVPSQSWTIPREQFTMDKLLINGTKGRPLWSSVSNLETOKPDTPQI 128  
DB 74 RSNKTQTVAAAGRSWAIIPREQLTMSDKLLVWGTRKAGQPLWPPVFVNLETOKPNAPRL 133  
QY 129 FSQVDISEATLEATVQWAPPVMPQKALTCQFRYKCEQAEAWTRLEPOLKTDGLTPVEM 188  
DB 134 GPDVDFSEDDPLEAVVHMAPPTWPSHKVLICQFHRRQEAATWLEPELKTPIPTPVEI 193  
QY 189 QNLEPGTCYQVSGRCQVNGYPMGWSPLSFQTPFLDPEDVWVSGTVCEYSGKRAALL 247  
DB 194 ODLELATGVYKVGRCMEKEEDLWGENSPILSFQTPPSAPKDVWVSGNLGCTPGGEEPL 253  
QY 248 WVKDPRPCVQVYTWFGAGDITTTQEEVPCKSPVPAMWMAVVSNGNSTSWPTNL 307  
DB 254 LMKAPGPCVQVSYKVMFWVWVGRELSPGEGITCCSLIPSGAEWARYSAVNATSWEPNL 313



NAME: Parker, Gary E  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 636 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-275-925-5

Query Match 59.7%; Score 2044; DB 3; Length 636;  
Best Local Similarity 62.8%; Pred. No. 4.4e-171;  
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

9 LPTLELLLSLLSGTRPHGSPGLQCYSGVPLGILNCSWEPLDGLTTPPVLYHQSKY 68  
14 LPKALLPLLVLFQTRPQGSAGPLQCYGVPLGDLNCSWEPLDGLGAPSELHLSQSKY 73  
69 HPNRVWEVKVPSQSWVTIPREQFTMAKLLIWGTQKGRPLWSSVSNLETKMPPV 128  
74 RSNKQTQVAVAGRSWAIPREQLTMSDKLLVWGTKAGQPLWPPVFVNLETKMKNAPRL 133  
129 FSDVISEEATLEAVQWAPPVPPQKALTCQFRYKCOAEAWTRLEPOLKTDGLTPVEM 188  
134 GPDVDFSEDDPLEAVTHWAPPTWPSHKVLICQFHYRRCQEAATLLEPELKTIPTPVEI 193  
189 QNLEPGTCYQVSGRCQVNGYP-WGEWSSPLSFQTFDPEVDVWYSGTVCETSGKRAALL 247  
194 ODLELATCYKVYGRCKMEKEEDLWGENSPILSFQTPPSAPKDVWVYSGNLCTPGGEEPLL 253  
248 VVKDPRPCVQVITYWFGAGDITTTQEEVPCKSPVPAMWMAVSPGNSWPPPTNLS 307  
254 LKAPGPCVQVSYKVMFWVGGRELSPGEGTCCCLIPSGAENARVSAVNATSWEPNLNLS 313  
308 LVCLAPESAPCDVGVSSADGSPGKIVTKQGRKPLEYVVDWAQDGLDKLNWTRLPPG 367  
314 LVCLDSASAPRSVAVSSTAGSTELLVTWQPGGEPLHVVDWARGDPLEKLNWVRLPPG 373  
368 NLSTLLPGEGKGVPIRYTAVYSGGLAAAPSVNGFEELVPLAGPAWVRLPDDPGPTP 427  
374 NLSALLPGNFTVGVPIRYTAVSAGSLASASSVNGFEELVPLVGLPWLRLQDAPGPTP 433  
428 VVANGVPRHQLRGQATHYTCIQSRGLSTVCRNYSSTQTATLNLHSGSKFLWTVYST 487  
434 AIANGVPRHQLRGHLYTLCAQSGTSPSCMVNYSSTQSVTLTDLPMWPCLEWTVAST 493  
488 VAGQPPGPDLSLHLPDNRIRKALPWFILWGLLGMCGSLASTRCLQARCLHWRHKL 547  
494 IAGQPPGPILRLHLPDNTLRWKVLPGLFVLWGLFLGCGLSLATS-----GRCYHLRHV 549  
548 LPQWTRVDPDANSNGOPYKEYLSLPQPKDGPFILEVEEVELOPVVES---PKASAPI 604  
550 LPRWVWEKVPDANSNGOPHEQVPEAQLGDLFILEVEEVEPPPVMESSQAQATAPL 609  
605 YSGYEKHLPTPEELGLL 622  
610 DSGYEKHLPTPEELGLL 627

RESULT 7  
US-08-653-740-3  
Sequence 3, Application US/08653740  
Patent No. 5792850  
GENERAL INFORMATION:  
APPLICANT: James W. Baumgartner  
APPLICANT: Donald C. Foster  
APPLICANT: Frank J. Grant  
APPLICANT: Cindy A. Sprecher

TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/653,740  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 578 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-653-740-3

Query Match 54.5%; Score 1866.5; DB 1; Length 578;  
Best Local Similarity 61.7%; Pred. No. 1.5e-155;  
Matches 353; Conservative 53; Mismatches 153; Indels 13; Gaps 3;

9 LPTLELLLSLLSGTRPHGSPGLQCYSGVPLGILNCSWEPLDGLTTPPVLYHQSKY 68  
14 LPKALLPLLVLFQTRPQGSAGPLQCYGVPLGDLNCSWEPLDGLGAPSELHLSQSKY 73  
69 HPNRVWEVKVPSQSWVTIPREQFTMAKLLIWGTQKGRPLWSSVSNLETKMPPV 128  
74 RSNKQTQVAVAGRSWAIPREQLTMSDKLLVWGTKAGQPLWPPVFVNLETKMKNAPRL 133  
129 FSDVISEEATLEAVQWAPPVPPQKALTCQFRYKCOAEAWTRLEPOLKTDGLTPVEM 188  
134 GPDVDFSEDDPLEAVTHWAPPTWPSHKVLICQFHYRRCQEAATLLEPELKTIPTPVEI 193  
189 QNLEPGTCYQVSGRCQVNGYP-WGEWSSPLSFQTFDPEVDVWYSGTVCETSGKRAALL 247  
194 ODLELATCYKVYGRCKMEKEEDLWGENSPILSFQTPPSAPKDVWVYSGNLCTPGGEEPLL 253  
248 VVKDPRPCVQVITYWFGAGDITTTQEEVPCKSPVPAMWMAVSPGNSWPPPTNLS 307  
254 LKAPGPCVQVSYKVMFWVGGRELSPGEGTCCCLIPSGAENARVSAVNATSWEPNLNLS 313  
308 LVCLAPESAPCDVGVSSADGSPGKIVTKQGRKPLEYVVDWAQDGLDKLNWTRLPPG 367  
314 LVCLDSASAPRSVAVSSTAGSTELLVTWQPGGEPLHVVDWARGDPLEKLNWVRLPPG 373  
368 NLSTLLPGEGKGVPIRYTAVYSGGLAAAPSVNGFEELVPLAGPAWVRLPDDPGPTP 427  
374 NLSALLPGNFTVGVPIRYTAVSAGSLASASSVNGFEELVPLVGLPWLRLQDAPGPTP 433  
428 VVANGVPRHQLRGQATHYTCIQSRGLSTVCRNYSSTQTATLNLHSGSKFLWTVYST 487  
434 AIANGVPRHQLRGHLYTLCAQSGTSPSCMVNYSSTQSVTLTDLPMWPCLEWTVAST 493  
488 VAGQPPGPDLSLHLPDNRIRKALPWFILWGLLGMCGSLASTRCLQARCLHWRHKL 547  
494 IAGQPPGPILRLHLPDNTLRWKVLPGLFVLWGLFLGCGLSLATS-----GRCYHLRHV 549

<b>QY</b>	<b>548</b>	LPOWIWVPDPANNSGQPYIKEVSLPQPPK	<b>579</b>
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<b>D6</b>	<b>550</b>	LPRWYEKVDPDANSSSG-----LLGPFR	<b>573</b>

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RESULT      8
US-09-073-594-3
; Sequence 3, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,594
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 578 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-073-594-3

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Try Match	54.5%	Score 1866.5	DB 2	Length 578
Best Local Similarity	61.7%	Pred. No. 1.5e-155		
Matches 353; Conservative	53	Mismatches 153	Indels 13	Gaps 3

Qy	9	LTPLELLLSLMSLLLRPHGSGPGLQCYSGVPLGLTNCWEPGLGDELTTPPVLYHQSQKY	68
Db	14	LPKLALLPLLWJLFQRTPOGSAGPLQCYGVGPLGDLNCWEPGLGDLGAPSELHLSQSKY	73
Qy	69	HPNRVMEVKVPSKQSWYTPREQFTWADKLLTWGTQKGRPLKSSVSVNLETKWMDPTPOI	128
Db	74	RSNKTTQTVAAAGRSWAIPREQULTMSDKLLVWGTGAGQPLPPVFPVNLETKMKNAPRL	133
Qy	129	FSQVDTSEETLEATVOWAPPVPPQKALTCQPRYKEQCAEWATRLPEQLKTDGLTPVPM	188
Db	134	GPVDSEDDPLEATVHWAPPTWPSHKVLIQCQPHYRCQEAATWLEPELKIPTLPVEI	193
Qy	189	QNLPGTCYOVSGRCOVENYCP-WGWSWSPSLSPOTFLDPEDWVSGTCVETSGKRAALL	247
Db	194	QDLELATGYKYGRCRMEXEEDLGEWSPILSFQTPPSAPKDVWVSGNLCCTGPGGEPLL	253
Qy	248	VKWDPRPCQVQVTVVWFGAGDITTTQEEVPCCKSPVPAHMEWAVYSPGNSTSWPPTNLUS	307
Db	254	LWRAPGCPGVSYKVWFVWGGREISPEGITCCCSLLTSPGAEARVAVSAVATSWEPITNLUS	313

Qy	308	LVCLAPESACDVCVSSADSGPGIKVYTWKOGTKRKPLEYVVDVMAQDGDSDLKLNWLRPLPG	367
Db	314	LVCLDSASPRSAVSSVAGSTELLVYTWQPGCEPLEYHVVDVMAQDGDPLEKLNWLRPLPG	373
Qy	368	NLSLLPCEKGGVPYRITVTAVYSGCLAAAPSVWGFREELVPLAGPVMVRLPDDPGPTP	427
Db	374	NLSALLPGNFTVGPYRITVTAVSASGLASASVWGFREELVPLGPTLWRLQDAPPGTP	433
Qy	428	VVANGVPRHQLRQQAHYTFCIQSRGLSTVYCRNVSSQGTATLPNLHSGSFYKLVTVST	487
Db	434	AIANGVPRHQRLGHLHYTLCAQSGTSPSCVMNVSGNTQSVTLPLDLPWGPCELVWTAST	493
Qy	488	VAGOGPGPDLSLHLPDNRIRWALPWFLSLWGLLWGCGLSLASTPCLQACRLHWRHKL	547
Db	494	IAGOGPGPIRLHLPLDNTLRWVLPGLFWGLFLWGCGLSLATS-----GRCYHLRHVK	549
Qy	548	LPQWIWVERVDPDPAANSNSGQPIYKEVSLPQPPK	579
Db	550	LPRVWPKVDPDPANSSSG-----LLGPPR	573

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RESULT          9
US-09-275-925-3
; Sequence 3, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/275,925
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 578 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-275-925-3

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Query Match	Score	DB 3	Length
Best Local Similarity	54.5%	1866.5	578
Matches	61.7%	pred. NO. 1.5e-155	
Conservative	53	Mismatches 153	Indels 13
			Gaps 3

[illegible]

Db 74 RSNKTTQTVAVAGRSWAIPREQLTMSDKLLVWGTKAGQPLPVPVFNLETKMKNAPRL 133  
Qy 129 FSOVDISEATLEATVONAPWPPQKALTCOFRYKECOAEATRLRLPOLKTDGLTPVEM 188  
Db 134 GPDVDFSEDDPLEATVHAPTWPSHKVLICQFHYRCQEAATWLLLELTKTIPLTPEI 193  
Qy 189 QNLEPGTCYVSGRCQVNGYP-NGEWSPLSFOTPFLOPDDVWVSGTVCETSGKRAALL 247  
Db 194 QDLELATGYKYVGRMEKEEDLWGEWSPILSFOTPPSPAPKDVWVSGNLCTPGGEPL 253  
Qy 248 WKOPRCVQVYIYWFAGDITITTOEVPCKSPVPANMEWAVVSPONSTSWPPTNLS 307  
Db 254 LKAPGPCVQVSKVWFVGGRELSPEGITCCCLIPSGAEWARSAYNATSWELTNLS 313  
Qy 308 LVCLAPASPCDVGSSADGPGIKTRKPLEVVDVWAOGDSDLKLNTRLP 367  
Db 314 LVCLDSAPRSVAVSSITAGSTELLVTHQPGPELEHVVDWARDGDPLEKLNWVRLPP 373  
Qy 368 NLSTLLPGEFGVYRITVAVYSGGLAAAPSVMGFREELVPLAGPAVWRLPDDPGTP 427  
Db 374 NLSALLPGNFTGVYRITVAVSASGLASASSVGMFREELAPLVGPTLWRLQDAPGTP 433  
Qy 428 VVANGEVPRHQLRGQATHYTCIOSRGLSTVCRNVSSOTQATLPLNLSGSEFKLWTVST 487  
Db 434 AIANGEVPRHQLRGHLTHYTLCAOSGTSPSCMVNMGNTQSVTLPLDLPWGPCELWVTAST 493  
Qy 488 VAGOGPGDLSLHLPDNRIRKALPWFSLWGLLMLGCGLSLSTRCLQARCLHWRHKL 547  
Db 494 IAGOGPGPILRLHLPDNLKWLKVLPGTLFLWGLFLGCGLSLATS-----GRCHLRHKV 549  
Qy 548 LPQNIWKPDPANSGQPYKEVSLPQPK 579  
Db 550 LPRVWKEVDPANSSG-----LILGPR 573

RESULT 10  
US-08-685-118-2  
; Sequence 2, Application US/08685118  
; Patent No. 5840530  
; GENERAL INFORMATION:  
; APPLICANT: Gubler, Ulrich A  
; APPLICANT: Presky, David H  
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/685,118  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silverman, Robert A.  
; REGISTRATION NUMBER: 35,682  
; REFERENCE/DOCKET NUMBER: CD 9195  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201) 235-2863  
; TELEFAX: (201) 235-2363  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 862 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-685-118-2  
Query Match 11.2%; Score 384; DB 2; Length 862;  
Best Local Similarity 25.1%; Pred. No. 3.8e-25;  
Matches 171; Conservative 88; Mismatches 281; Indels 140; Gaps 33;  
Qy 5 RVARUTPLELLLSLMSLLGTRPHSGPGPLOCYSYVGLGILNCSEPLGD--LETPPVLY 62  
Db 102 KLACINSDEIQICGAEIFGVNAPE-QPNLSCIOQGEQGTACTWGERDTHLYEYTLQ 160  
Qy 63 HQSQYHNRNWEVK-----VPSKOSWVTIPREQFTMDKLLIMGTOKGR 107  
Db 161 LSGPK---NLTWQCKDIYCDYDFGINLTPE-----PESNFTAKVTAV-----N 204  
Qy 108 PLWSSVSNLETKMPTQPFQSFQVDISEEATLEATVQWAPVWPP-----QKA----- 156  
Db 205 SLGSSSL-----PSTFTFLDI-----VRPLPP-WDIRIKFKQKASVSRCTL 244  
Qy 157 -----LTCOFRYKECOAEATRLPOLKTDGLTPVEMONLEPGTCV--QVSGRCOVE 206  
Db 245 YWRDEGLVLLNLRVPSNSRLNWNV---VTKAGRHDLDLKFTTEYEFQISSKLHL 301  
Qy 207 NGYPMGEWSPLSFOTPFDPPE---DVWVSGTVCETSGKRAALLVWK-----DPRPCV-- 256  
Db 302 KG-SWSDNSESLSRAQTPPEEPTGLDVMYMKRHIDYSRQISLF-WKNLSVSEARGKILH 359  
Qy 257 -QVITYWFGAGDITITTOEVPCKSPVPANMEWAV-VSPGNSTSWPPTNLS--VCLA 312  
Db 360 YQVTLQELTGKAMQNTITGHTSMVTIVPTGNWAVAVSAANSKSSSLPTRINIMNLCEA 419  
Qy 313 PESAPCDVGVSSADGSPGIKVTQKGRKP---LEVYVDAQ---DGDSDLKLNTRLP 366  
Db 420 GLLAPQVANS-EGMDNLTWPPKDPKDPNAVQYVYVWEHLHGGDTQVPLMWLRSP 478  
Qy 367 GNLSTLLPGEFGVYRITVAVYSGGLAAAPSVMGFREELVPLAGPAVWRLPDDPGT 426  
Db 479 YNVSALISENIKSYICYEIRVVAL-SGDOGGCSSILGSKHKKAPLSGPHNAITEE-KGS 536  
Qy 427 PVVANGEVPRHQLRGQATHYTCIOSRGLSTVCRNVSSOTQATLPL-----NLH----- 475  
Db 537 ILISWNSIPVQEQMCGLLHYRIYKWE-----RDSNSQQLCEIPYRVSONSHPINSLQ 589  
Qy 476 -SGSFKLWVTVSTVAGQPGPDLSLHLPDNRIRKALPWFSLWGLLMLGCGLSLSTR 534  
Db 590 PRVTVLWMTALTAAAGESHGNREFECL-QKANWMAFVAPISICIAIIVWG-----IFSTH 644  
Qy 535 CLQARCLHWRHKLPLQWNIWVDPDPANSGQPY-IKEVSLPQP-----PKDGP 583  
Db 645 YFOQKVFVLLAALRPQWCSREIPDPANSTCAKYPVIAEKTQLDLRLIDWPTDEPPEP 704  
Qy 584 LEVEEV--ELOPVVESPKAS 601  
Db 705 LVISEVLHQVTPVFRHPPCS 724  
RESULT 11  
US-08-915-495-2  
; Sequence 2, Application US/08915495  
; Patent No. 5852176  
; GENERAL INFORMATION:  
; APPLICANT: Gubler, Ulrich A  
; APPLICANT: Presky, David H  
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07110

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/915,495
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE:
; FILING APPLICATION NUMBER: 08/685,118
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 862 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-915-495-2

Query Match 11.28; Score 384; DB 2; Length 862;
Best Local Similarity 25.18; Pred. No. 3.8e-25;
Matches 171; Conservative 88; Mismatches 281; Indels 140; Gaps 33;

Qy 5 RVARLTPELLLSLLSLGTRPHGSPGLQCYSGPLGILNCWEPLGD--LETPPVLY 62
Db 102 KLACINDEIQICGAEIFVGVAPE-QPNQLSCIQKGEQGTVACIWERGRDTHLYEYTLQ 160
Qy 63 HQSKYHNPRVWEVK-----VPSKOSWVTIPREOFTMADKLLMGTKRGR 107
Db 161 LSGPK--NLTWQCKDIYCDYDFGINLPES-----PESNFTAKVTAV-----N 204
Qy 108 PLWSSVSNLETQMKPDPPQIFSQVDISEATLEATVQWAPVPVPP--QKA----- 156
Db 205 SLGSSSL-----PSTFTFLDI-----VRPLPP-WDIRIKFOKASVSRCTL 244
Qy 157 -----LTCQFRYKEQCAEWRLERPLQKTDGLTPTVEMONLEPGTCY--QVSGRCOVE 206
Db 245 YWRDEGLVLLNRLRYRPSNSRLNNVN--VTKAKGRHDLDLKPFTEYEQISKKLHLY 301
Qy 207 NGYPWGENSSPLSFOTPELPDPE---DVWSGTCTGCTSKRAALLVWK-----DPRPCV-- 256
Db 302 KG-SWSOWSESILRAQTPEEPTGMLDVWYMKRHIDYSRQISLFL-WKNLSVSEARGKILH 359
Qy 257 -QVITYTWFGAGDITTTQEEVPCCKSPVPAMWEMAV-VSPGNSTSWPPTNLSL--VCLA 312
Db 360 YQVTLQELTGCKAMTQNTIGHTSWTTPRTGNWAVASAAKSGSLPTRINIMNLCEA 419
Qy 313 PESAPCDGVGSADGSPGICKYTWQGRKRP---LEYVVDWAQ---DGSDLKLNWTRLP 366
Db 420 GLLAPRQVSANS-EGMDNILLTWQPPKDPKPSAQVEYVYVWEHLHPGGDTQVPLNWLRSRP 478
Qy 367 GNLSTLLPGEPKGGVYPRITVAVYSGGLAAPSVMGFEELVPLAGPAVWRLPDDPGT 426
Db 479 YNVSALISENIKSYICYEIRYVAL-SGDQGCSSILGNSKKHAPLSGPHINAITEE-KGS 536
Qy 427 PVVANGVPRHLRGQATHYFCIQSRLSTVCRNVSSQTATPL-----NLH----- 475
Db 537 ILISWNSIPVQEQGLLHYRIYKE-----RDSNSQQLCEIPYRVSONSHPINSLQ 589
Qy 476 -SGSFKLWVTYSTVAGOGPPGPDILSLHLPDNRIRWAKLPWFLSLWGLLLMCGLSASTR 534
Db 590 PRVTYVLMNTALTAAEGSSHNEFECL-QQKANMAFVAPISCIATIIIMVG-----IFSTH 644
Qy 535 CLQARCLHWRHKKLPQWIWERVDPDPSNNSQCPY-IVEVSLPOP-----PKDGP 583

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Db 302 KG-SWSDSESRAGQPEEBEPTGMDLVWYMKRHIDYSROOISLF-WKNLSVSEARGKILH 359  
QY 257 -QVTVWFAGDITTOEBEPCCKSPVPAWMEWAV-VSPGNSTSWPPTNLNL--VCLA 312  
Db 360 QYVTLQELTGKAMQNTGHTSWTIPRTGNWAVASAAKSGSLPTRINIMNLCEA 419  
QY 313 PESAPCDGVSSADSGPGKVTWKGTGRKP----LEYVDMAQ---DGDSDLKLNWTRLP 366  
Db 420 GLLAPRQVSANS-EGMDNLTWQPPRKDPSAVQEVVVEWREHLPGDGTQVPLNMLRSR 478  
QY 367 GNLSLTLLPCEFGKGVYRTVTAVYSGGLAAAPSVMGPFREELVPLAGPAVWRLPDDP 426  
Db 479 YNVSALISENIXSYCYEIRVAL-SGOGGCSILGNSKHAPLSGPHINAITEE-KGS 536  
QY 427 PYVAMEGVRHQLRGQATHYFCIQSGLSTVCRNVSSQOTATLP-----NLH----- 475  
Db 537 ILISNNSIPVQOMGCLLHYRYWKE-----RUSNQPQLCEIPRYVSONSHINSIQ 589  
QY 476 -SGSKLWTVSTVAGQGGPPDLSLHLPDNIRKALPWFSLWGLLLMGCGLSLASTR 534  
Db 590 PRVTYVLMTALTAAAGESSHNEREFCL-QGKANWMAFVAPSICTAIINVG----IFSTH 644  
QY 535 CLQARCLHWRHKLLOQWIERVPDANSNGOPY-IKEVSLPQ-----PKDGP 583  
Db 645 YFQKVVFVLLAALRQWMSREIPDPANSTCAKKYPIAEKTLQPLDLRLIDWPTPEDPEP 704  
QY 584 LEVEEV--ELQPVVESPKAS 601  
Db 705 LVISEVLHQTVPFRHPPCS 724

RESULT 13

US-08-419-652-7  
; Sequence 7, Application US/08419652  
; Patent No. 5831007  
; GENERAL INFORMATION:  
; APPLICANT: Chua, Anne O  
; APPLICANT: Gubler, Ulrich A  
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: United States of America  
; ZIP: 07110-1199  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: PC compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/419,652  
; FILING DATE: 11-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,532  
; FILING DATE: 31-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/094,713  
; FILING DATE: 19-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kass, Alan P  
; REGISTRATION NUMBER: 32142  
; REFERENCE/DOCKET NUMBER: CD 9174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201) 235-4205  
; TELEFAX: (201) 235-3500  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 620 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..620  
; OTHER INFORMATION: /note= "Represents residues 331 to  
; OTHER INFORMATION: 950 of leukemia inhibitory factor-  
; OTHER INFORMATION: receptor..."  
; US-08-419-652-7

Query Match 8.1%; Score 277; DB 2; Length 620;  
Best Local Similarity 21.7%; Pred. No. 5.8e-16;  
Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

QY 27 PHGSGPLOCYSGVGLIILNCSEWEP-----LGDLETPPVLYHQ-SOKYHPRHWEVKVP 79  
Db 2 PDPTQQLNC-ETHDLKEIICSMNPGRVTAALGPRATSYTLVESFSGKY--VRLKRAEAP 58  
QY 80 SKOSW---VTIPREQ---FTMADKLLINGTKGRPL---WSSVSVNLETKMPPDTPQIF 129  
Db 59 TNESYQLLFQMLPQEIYNTL-----NAHNPGLRSQSTILWNITEKYVPHPTSF 109  
QY 130 SQVDISEEATLEATVQWAPPVPPQKALTCQPRYKCAEAWTRLEPOLKTDGLTP---- 185  
Db 110 KVKDINSTA---VKLSWHLPGNFAKINFLECEIEIKKNS---VQEQRNVTIKGVENSYL 163  
QY 186 VEQNLEPGTCYQVSGRCQVNGYPMGEMSSPLSQTPFLDPE---DVMVGTVCTSGK 242  
Db 164 VALDKLNPYTLTFRICSTETFWKWSKNSKKQHLJTTEASPSKPDWTREWS---SDGK 220  
QY 243 RAALLWKDPRPCVO-----VTYVMFGAGDITTTQEEVPCCKSPVPAWNE-----WAVV 292  
Db 221 N-LIIYWK-PLPINEANGKILSYNVSCSDEETQSLSEIPDPQHKAEIRLDKNDYIISV 278  
QY 293 SPGNSTSWPPTNLVLCLAPESAPCDVGVSSADG-SPGIKVTWKQGTGRKPLEYVVDMAQ 351  
Db 279 AK-NSVGSSPPSKIA-----SMEIPDDLKIEQVGVGKGIILLTWHYDPNMTCDYVIKWCN 333  
QY 352 DGDSDLKL-NWTRLPNGLSTLLPG-EFKGGVYPIRTVTAVYSGGLAAAPSVMGPFREELV 409  
Db 334 SSRSEPCLMWRKVPNSSTETVIESDEFPRGIRYNFLYGCGRNQGYQLLRSMIGYIELA 393  
QY 410 PLAGPAVWRLPDDPPTGTPVWAMEGVRHQLRGQATHYF-----CIGSRGLS 456  
Db 394 PIVAPN-FVIEDTSADSLVWKWEDIPVELRGFLRGYLEYFGKGERDTSKMRVLESGRSD 452  
QY 457 TVCRNVSSQO-TATLPNLH-SGSFKLWTVSTVAGQGGPPDLSLHL--PDNIRMKAL 512  
Db 453 IKVKNITDISQKTLRIADLQGTSYHLVLRVAVT---DGGVGPEKSMYVVTKENS----- 504  
QY 513 PWFLSLWGLL-----LMGCGLSLASTRCLQARCLHWRHKLLOQWIER-----VP 557  
Db 505 -----GLTIIAILPVAIVGV---VTSILCYRKR-----EMIKETFPDIP 544  
QY 558 DPANSNS-----GOPYIKEVSL-POPKDGPTE-----VEEVE-LQPVVESPK 599  
Db 545 NPENCKALQFQKSVCEGSSALATLEMNCTPNNVEVLETRSAFPKIEDTEIISPVAERPE 604

RESULT 14

US-07-797-556-6  
; Sequence 6, Application US/07797556  
; Patent No. 5262522  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street

; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/797,556  
; FILING DATE: 19911122  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2607  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; TELEFAX: 206-587-0606  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1001 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-797-556-6

Query Match 8.1%; Score 277; DB 1; Length 1001;  
Best Local Similarity 21.7%; Pred. No. 1.2e-15;  
Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

QY 27 PHGSPGLOQYCVSGVGLILNCSEWEP-----LGDLETPPVLYHQ-SQKYHPNRVMEVKVP 79  
DB 332 PPTPQQLNC-ETHDLKEICSNMGRVYALVGPRTATSLVSEFSQKY--VRLKRAEAP 388  
QY 80 SKQSW-----VTIPRQ---FTMADKLLINGTQKGRPL---WSSVSVNLETQMKPDPQTQIF 129  
DB 389 TNEYSQLLFQMLPQNEIYNFTL-----NAHNPLGRSQSTILVNITEKVPYHPTPTSF 439  
QY 130 SQVDISEATLEATVQWAPPVPPQKALTCQFPRYKCAQAEWTRLEPQLKTDLTP---- 185  
DB 440 KVKDINSTA---VKLSMHLPGNFAKINFCEIEIKKNS---VQEQRNVTIKGVNSSYL 493  
QY 186 VEMQNLPEPTCYQVSGRCQVNGYPMGWSPLSFQTPFLDPE---DVMVSGTVCETSGK 242  
DB 494 VALDKLNPYTLTYFRIRCSSTETFEWKSNNKQHLTTEASPSKGPDTWREWS---SDGK 550  
QY 243 RAALLVWKDPRPCVQ-----VTYTVWFGAGDITTTQEEVPCCKSPVPAMWE-----WAVV 292  
DB 551 N-LIIYWK-PLPINEANGKILSYNVSCSSDEETQSLSEIPDPQHKAEIRLDKNDYIISV 608  
QY 293 SPGNSTSWPPTNLSLVCLAPESAPCDGVSSADG-SPGIKVTWKQGRKPLEYVVDNAQ 351  
DB 609 AK-NSVGSSPPSKIA-----SMEIPNDLLKIEQVGMGKILLTWHYDPNMTCDYIKWCN 663  
QY 352 DGDSDLKL-NWTRLPNGNLSTLPG-EFKGGVPYRITTVAVYSGGLAAAPSVMGPREELV 409  
DB 664 SSRSEPLMDWRKVPNSTETVIESDEFGRGTYNFFLGCNRQNGQLRLSMIGYIEELA 723  
QY 410 PLAGPAWRLPDDPGTTPVAVNGEPRHOLRGOATHYF-----CIGSRGLS 456  
DB 724 PIVAPN-FTVEDTSADSLVKMEDIPVEELRGLFRLGYLFYFGKGERDTSKMRVLESGRSD 782  
QY 457 TVCRNVSSOTO-TATLPNLH-SGSFKLWTVSTVAGOGPPGPDLSLHL--PDNRIRWAKL 512  
DB 783 IKVKNLTDISQKTLRTADIQGTSTHVLVIRAYT---DGGVGPEKSPVYVTKNSV----- 834  
QY 513 PMFLSLWGLL-----LMGCSLSASTRCIQAARCLHNRHKLLOWIWER-----VP 557  
DB 835 -----GLIIALLIPVAVAVIGV---VTSILCYKR-----EWIKETYPDP 874

QY 558 DPANSNS-----GQPYIKVEVSL-POPPKDGPILE-----VEEVE-LQPVVESP 599  
DB 875 NPENCKALQFQKSVCGSSALKLTLENNPCTPNNVEVLETRSAPFKIEDTIIISVPAERPE 934  
RESULT 15  
US-07-943-843-2  
; Sequence 2, Application US/07943843  
; Patent No. 5284755  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; APPLICANT: Beckmann, M. P.  
; TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/943,843  
; FILING DATE: 19920911  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2606-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; TELEFAX: 206-587-0606  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1001 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-943-843-2

Query Match 8.1%; Score 277; DB 1; Length 1001;  
Best Local Similarity 21.7%; Pred. No. 1.2e-15;  
Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

QY 27 PHGSPGLOQYCVSGVGLILNCSEWEP-----LGDLETPPVLYHQ-SQKYHPNRVMEVKVP 79  
DB 332 PPTPQQLNC-ETHDLKEICSNMGRVYALVGPRTATSLVSEFSQKY--VRLKRAEAP 388  
QY 80 SKQSW-----VTIPRQ---FTMADKLLINGTQKGRPL---WSSVSVNLETQMKPDPQTQIF 129  
DB 389 TNEYSQLLFQMLPQNEIYNFTL-----NAHNPLGRSQSTILVNITEKVPYHPTPTSF 439  
QY 130 SQVDISEATLEATVQWAPPVPPQKALTCQFPRYKCAQAEWTRLEPQLKTDLTP---- 185  
DB 440 KVKDINSTA---VKLSMHLPGNFAKINFCEIEIKKNS---VQEQRNVTIKGVNSSYL 493  
QY 186 VEMQNLPEPTCYQVSGRCQVNGYPMGWSPLSFQTPFLDPE---DVMVSGTVCETSGK 242  
DB 494 VALDKLNPYTLTYFRIRCSSTETFEWKSNNKQHLTTEASPSKGPDTWREWS---SDGK 550  
QY 243 RAALLVWKDPRPCVQ-----VTYTVWFGAGDITTTQEEVPCCKSPVPAMWE-----WAVV 292  
DB 551 N-LIIYWK-PLPINEANGKILSYNVSCSSDEETQSLSEIPDPQHKAEIRLDKNDYIISV 608  
QY 293 SPGNSTSWPPTNLSLVCLAPESAPCDGVSSADG-SPGIKVTWKQGRKPLEYVVDNAQ 351  
DB 609 AK-NSVGSSPPSKIA-----SMEIPNDLLKIEQVGMGKILLTWHYDPNMTCDYIKWCN 663





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